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                DEL HIS
                E DE96-19632521/AP,PRN
L1            1 S E3,E4
                E DE97-19725362/AP,PRN
L2            1 S E4
                E WO97-EP4396/AP,PRN
L3            1 S E3,E4
L4            1 S L1-L3
                E FORSSMAN/AU
L5          272 S E10-E16
                E SCHULZ KNAPPE/AU
L6           51 S E5,E6
                E SCHULZ KNAP/AU
                E SCHRADER M/AU
L7           77 S E3-E7,E18-E20
                E OPITZ H/AU
L8           57 S E3-E4,E9-E11
                E BIOVIS/PA,CS
L9            2 S E5-E8
L10         400 S L5-L9
L11          30 S L10 AND 9/SC
L12           9 S L10 AND 9/SX
L13          39 S L11,L12
L14          21 S L13 AND (PROTEIN# OR PEPTIDE#)/CW
L15           3 S L13 AND (PROTEIN# OR PEPTIDE#)/CW (L) (ANT OR PUR OR ANST OR
L16          18 S L14 NOT L15
L17       84590 S (PROTEIN# OR PEPTIDE#)/CW (L) (ANT/RL OR ANST/RL OR OCCU/RL O
L18       13658 S (PROTEIN# OR PEPTIDE#)/CW (L) ANALYSIS/CW
L19          16 S L17,L18 AND L13
L20          20 S (?CHROMATOG? OR ?SPECTROM?) AND L13
L21          14 S L20 AND L15,L19
L22           3 S L4,L15
L23          11 S L21 NOT L22
L24           9 S L23 AND 9/SC
L25          12 S L22,L24
L26           9 S L16,L19 NOT L25
L27           3 S L10 AND LOW MOLECULAR WEIGHT
L28           1 S L27 AND L13
L29           2 S L27 NOT L28
L30           3 S L22,L28
L31          18 S L25,L26 NOT L30
L32       14268 S L17,L18 AND (?CHROMATOG? OR ?SPECTROM?)
L33        8281 S L32 AND 9/SC
L34         141 S L33 AND LOW MOLECULAR WEIGHT
L35           4 S L34 AND (PROCARYOT? OR EUCARYOT? OR MULTICELL? OR TISSUE)
L36           4 S L34 AND TRANSFORM?
L37           7 S L35,L36
L38           4 S DIAGNOS? AND L34
L39           5 S L34 AND (URINE OR BLOOD OR BODY FLUID)/CT
L40          14 S L37-L39
L41          18 S L31 NOT L40

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L40 ANSWER 1 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1998:126411 HCAPLUS
DN 128:164730
TI Process for determining the status of an organism by peptide pattern determination using **chromatography** and mass **spectrometry**
IN Forssmann, Wolf-Georg; Schulz-Knappe, Peter; Schrader, Michael; Opitz, Hans-Georg
PA Forssmann, Wolf-Georg, Germany; Schulz-Knappe, Peter; Schrader, Michael; Opitz, Hans-Georg
SO PCT Int. Appl., 24 pp.
CODEN: PIXXD2
DT Patent
LA German
IC ICM G01N033-68
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 6, 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9807036	A1	19980219	WO 1997-EP4396	19970813
	W: AL, AU, BA, BB, BG, BR, BY, CA, CN, CU, CZ, DE, EE, GE, HU, IL, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, SL, TR, TT, UA, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	DE 19632521	A1	19980219	DE 1996-19632521	19960813
	AU 9742988	A1	19980306	AU 1997-42988	19970813
	EP 922226	A1	19990616	EP 1997-918977	19970813
	R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE, PT, IE, SI, LT, LV, RO				

PRAI DE 1996-19632521 19960813
DE 1997-19725362 19970616
WO 1997-EP4396 19970813
AB The invention concerns a process to det. the status of an organism by measuring peptides in a sample of the organism which contains high-mol.-wt. and **low-mol. wt.** peptides; the pattern of the low-mol.-peptides acts as an indicator of the organism's status when compared to ref. peptide patterns. Body fluids, **tissues** or whole organisms can be analyzed. **Low-mol.-wt.** peptides up to 30 kDalton, but preferably between 100 and 10,000 Dalton are first isolated e.g. by ultrafiltration and than sepd. by gel filtration, reverse phase **chromatog.** etc.; fractions are collected and analyzed by mass **spectrometry**, e.g. MALDI, electrospray ionization mass **spectrometry**. Thus, a pattern reflecting mol. wt., **chromatog.** behavior, etc., is obtained and this pattern is compared to peptide patterns of ref. sources. **Transformed** microorganisms can be compared to wild types and body fluids of sick or medicated patients can be compared to healthy individuals. Thus, blood-derived filtrate was applied to a **chromatog.** column and fractions were collected with seven

different eluents having pH values from 3.6 to 9.0. The fractions were sep. applied to a reverse-phase column and the 4 mL fractions were further sepd. with a microbore reverse-phase column; UV detection and online electrospray ionization mass **spectrometry** were used in the pos. ion mode. The fractions were also analyzed in a MALDI using an L(-)fucose matrix. The pattern of peptides was compared to databanks, e.g. Swiss-Prot and EMBL.

ST organism peptide pattern **chromatog** mass spectroscopy

IT Ascites
Blood analysis
Body fluid
Chromatography
Diagnosis
Electrospray ionization mass **spectrometry**
Gel permeation **chromatography**
Matrix-assisted laser desorption ionization mass **spectrometry**
Microorganism
Reversed phase **chromatography**
Transformation (genetic)
Ultrafiltration
Urine analysis
(process for detg. status of organism by peptide pattern detn. using **chromatog.** and mass **spectrometry**)

IT **Peptides, analysis**
RL: **ANT (Analyte)**; BOC (Biological occurrence); **PUR (Purification or recovery)**; **ANST (Analytical study)**; BIOL (Biological study); **OCCU (Occurrence)**; PREP (Preparation)
(process for detg. status of organism by peptide pattern detn. using **chromatog.** and mass **spectrometry**)

L40 ANSWER 2 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:564457 HCAPLUS
DN 125:241979
TI Direct-injection HPLC: **Chromatography** of biofluids without protein removal
AU Anderson, David J.
CS Department Chemistry, Cleveland State University, Cleveland, OH, 44115, USA
SO Methodol. Surv. Bioanal. Drugs (1996), 24(Biofluid Assay for Peptide-Related and Other Drugs), 183-193
CODEN: MSBDE6
DT Journal; General Review
LA English
CC **9-0** (Biochemical Methods)
AB A review with 33 refs. Several investigators have devised ways to allow direct injection of protein-contg. samples in the RP-HPLC anal. of **low mol. wt.** analytes. The two approaches, used, pre-column and raM* techniques, are now reviewed, with crit. assessment of the advantages and disadvantages of each.
ST review HPLC **chromatog** biofluid protein
IT **Body fluid**
(direct-injection HPLC: **chromatog.** of biofluids without protein removal)
IT **Proteins, analysis**
RL: ARU (Analytical role, unclassified); **ANST (Analytical study)**
(direct-injection HPLC: **chromatog.** of biofluids without protein removal)
IT **Chromatography**, column and liquid
(high-performance, direct-injection HPLC: **chromatog.** of biofluids without protein removal)

L40 ANSWER 3 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:272077 HCAPLUS
DN 125:4874
TI Micropreparative gel electrophoresis of **low-molecular-weight** peptides: purification of highly insoluble amyloid peptide

fragments
AU Baumann, Marc; Golabek, Adam; Lalowski, Maciej; Wisniewski, Thomas
CS Departments Pathology Neurology, New York Univ. Medical Center, New York, NY, 10016, USA
SO Anal. Biochem. (1996), 236(2), 191-8
CODEN: ANBCA2; ISSN: 0003-2697
DT Journal
LA English
CC **9-7** (Biochemical Methods)
AB We have used the continuous-elution micropreparative gel electrophoresis device described by Baumann and Lauraeus (Anal. Biochem. 214, 142-148, 1993) to purify **low-mol.-wt.** peptide fragments from in-gel digested std. proteins as well as highly insol. amyloid peptides. Alzheimer's amyloid .beta.-peptide, gelsolin-derived amyloid peptide of the Finnish type, and a novel amyloid of the British type were purified from either homogenized brain or kidney **tissue** material to a high degree of purity in a single run. Using the high resolving capacity of the Tris-Tricine-SDS buffer system of Schaegger and von Jagow (Anal. Biochem. 166, 368-379, 1978) were were able to isolate two synthetic peptides with Mr 4329 and 3284, differing only by 1045 in mass. The total peptide recovery, as detd. by amino acid sequence anal. and scanning densitometry, ranged between 60 and 80%. In order to demonstrate the utility of this technique we subjected some of the purified peptides to direct N-terminal amino acid sequence anal., mass **spectrometry**, microbore high-performance liq. **chromatog**., and immunochem. studies. Our results show that micropreparative gel electrophoresis is an effective tool for the isolation of not only larger polypeptides but also small peptide fragments in a form suitable for further biol. use.
ST amyloid peptide purifn gel electrophoresis
IT **Proteins**, specific or class, **analysis**
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(amyloid; micropreparative gel electrophoresis of **low-mol.-wt.** peptides and purifn. of highly insol. amyloid peptide fragments)
IT **Peptides, analysis**
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(micropreparative gel electrophoresis of **low-mol.-wt.** peptides and purifn. of highly insol. amyloid peptide fragments)

L40 ANSWER 4 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1995:487228 HCAPLUS
DN 122:260084
TI **Low molecular-weight** proteins in urine
AU Kuroda, Masayoshi
CS Med. Sch., Teikyo Univ., Japan
SO Kensa to Gijutsu (1994), 22(13), 1041-8
CODEN: KTGIDU; ISSN: 0301-2611
DT Journal; General Review
LA Japanese
CC **9-0** (Biochemical Methods)
AB A review with 9 refs. discussing anal. methods (electrophoresis, ion exchanger **chromatog.**, immunoassay, etc.) for and factors affecting the detn. of **low mol.-wt.** proteins in urine. Clin. applications of the methods. also are discussed.
ST review protein urine electrophoresis **chromatog** immunoassay
IT Ion exchangers
(column **chromatog.**; detn. of **low mol.-wt.** proteins in urine)
IT **Diagnosis**
Electrophoresis and Ionophoresis
Immunoassay
Urine analysis
(detn. of **low mol.-wt.** proteins in urine)
IT **Chromatography**, column and liquid

(ion exchanger; detn. of **low mol.-wt.** proteins in urine)

IT **Proteins**, specific or class
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(**low-mol.-wt.**, detn. of **low mol.-wt.** proteins in urine)

L40 ANSWER 5 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1995:412954 HCAPLUS
DN 122:155762
TI Method of sample preparation for urine protein analysis with capillary electrophoresis
IN Liu, Cheng-Ming; Wang, Hann-Ping
PA Beckman Instruments, Inc., USA
SO PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-483
ICS G01N033-493; G01N030-14; G01N027-447
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 13, 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9502182	A1	19950119	WO 1994-US5631	19940518
	W: CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 659274	A1	19950628	EP 1994-921199	19940518
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	CA 2143206	AA	19960119	CA 1994-2143206	19940518
	JP 08501638	T2	19960220	JP 1994-504023	19940518
PRAI	US 1993-91844		19930709		
	WO 1994-US5631		19940518		

AB Processes are provided for pretreating body fluid (e.g., urine) compns. and subsequently analyzing the pretreated body fluid compns. for analytes of interest esp. in clin. disease **diagnosis**. Processes for pretreating the compns. include providing a size exclusion gel having a mol. wt. fractionation range or a mol. wt. exclusion such that the size exclusion gel is capable of excluding or fractionating the analytes of interest and then causing the compn. to contact the size exclusion gel to sep. the analytes from **low-mol.-wt.** compn. components which interfere with the sepn. and anal. of the analytes of interest. Processes for analyzing pretreated compns. include electrophoretic methods such as capillary zone electrophoresis which involve the sepn. and detection of analytes of interest. Examples are given of the detn. of proteins in the urine of patients with myeloma and kidney disease.

ST urine protein detn gel **chromatog** electrophoresis; disease **diagnosis** protein detn urine pretreatment

IT **Chromatography**, gel
Diagnosis
Disease
Kidney, disease
Myeloma
Urine analysis
(proteins detn. in urine in disease by gel **chromatog.** and capillary electrophoresis)

IT Haptoglobins
Immunoglobulins
Transferrins
Albumins, analysis
Proteins, analysis
RL: **ANT (Analyte)**; THU (Therapeutic use); **ANST (Analytical study)**; BIOL (Biological study); USES (Uses)
(proteins detn. in urine in disease by gel **chromatog.** and

capillary electrophoresis)
IT Polysaccharides, biological studies
RL: NUU (Nonbiological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT Immunoglobulins
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Bence-Jones, proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT Proteins, biological studies
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(metabolic disorders, proteinuria, proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT Electrophoresis and Ionophoresis
(zone, capillary, proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT Macroglobulins
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(.alpha.2-, proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT Globulins, analysis
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(.gamma.-, proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT 9035-81-8, Trypsin inhibitor 9041-92-3, .alpha.1-Antitrypsin
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)
IT 9003-05-8, Polyacrylamide 9004-54-0, Dextran, biological studies
RL: NUU (Nonbiological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(proteins detn. in urine in disease by gel **chromatog**. and capillary electrophoresis)

L40 ANSWER 6 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1993:598899 HCAPLUS
DN 119:198899
TI Ultrahigh resolution matrix-assisted laser desorption/ionization of small proteins by Fourier-**transform** mass **spectrometry**
AU Castoro, John A.; Wilkins, Charles L.
CS Dep. Chem., Univ. California, Riverside, CA, 92521, USA
SO Anal. Chem. (1993), 65(19), 2621-7
CODEN: ANCHAM; ISSN: 0003-2700
DT Journal
LA English
CC **9-5** (Biochemical Methods)
AB Recent research has demonstrated that matrix-assisted laser desorption/ionization (MALDI) is feasible for Fourier-**transform** mass **spectrometric** anal. of biomols. with masses in excess of 50,000 Da. Here, the effects of electrostatic deceleration times and laser energy upon mass resoln. are reported. Optimum deceleration times for singly-charged MALDI-generated protein ions ranging in mass from 2627 to 29,000 Da are a linear function of m1/2 when a 9.5-V decelerating potential is used. Furthermore, higher resoln. is obtained with laser fluences close to the threshold for MALDI. Slow metastable decay of mol. ions in the absence of comatrix is demonstrated for melittin and bovine insulin. It appears that the resoln.-enhancing effect of comatrix may result from slowing mol. ion unimol. decompn. rates sufficiently to allow IR emission to compete with metastable decay, thus providing the requisite population of long-lived ions for high mass resoln. A spectrum of bovine insulin mol. ion with mass resoln. of 30,000 is presented, together with

several spectra of lower mass proteins with mass resoln. in excess of 100,000. Detection of a doubly-charged carbonic anhydrase trimer ion with a mass of 87,000 Da is reported.

ST small protein resoln mass **spectrometry**; Fourier **transform** mass **spectrometry** protein

IT Mass **spectrometry**
(Fourier-**transform**, ultrahigh resoln. matrix-assisted laser desorption/ionization of small proteins by, electrostatic deceleration times and laser energy effect on)

IT **Proteins**, specific or class
RL: **ANST (Analytical study)**
(**low-mol.-wt.**, matrix-assisted laser desorption/ionization of, ultrahigh resoln., by Fourier-**transform** mass **spectrometry**, electrostatic deceleration times and laser energy effect on)

IT 490-79-9, 2,5-Dihydroxybenzoic acid
RL: ANST (Analytical study)
(matrix contg., in ultrahigh resoln. matrix-assisted laser desorption/ionization of small proteins by Fourier-**transform** mass **spectrometry**)

IT 113-73-5, Gramicidin S 9001-03-0 9004-10-8, Insulin, biological studies 37231-28-0, Melittin 72711-43-4, .gamma.-MSH
RL: ANST (Analytical study)
(matrix-assisted laser desorption/ionization of, ultrahigh resoln., by Fourier-**transform** mass **spectrometry**, electrostatic deceleration times and laser energy effect on)

L40 ANSWER 7 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1993:208709 HCAPLUS
DN 118:208709
TI Profiling of endogenous brain peptides and small proteins: methodology, computer-assisted analysis, and application to aging and lesion models
AU Slemmon, J. Randall; Flood, Dorothy G.
CS Med. Cent., Univ. Rochester, Rochester, NY, 14642, USA
SO Neurobiol. Aging (1992), 13(6), 649-60
CODEN: NEAGDO; ISSN: 0197-4580
DT Journal
LA English
CC **9-3** (Biochemical Methods)
Section cross-reference(s): 13, 14

AB Significant advances in the technol. for the isolation of peptides and small proteins have permitted their identification as biol. markers and enhanced the study of the posttranslational life of proteins. The protocol described here examd. large nos. of **tissue**-derived peptides and small proteins, extd. in low pH and boiled so that proteolysis was interrupted. These were then fractionated batchwise by using size exclusion and ion-exchange **chromatog.** Profiles of species in the peptide pools were then generated by reversed-phase HPLC. The HPLC profiles were evaluated with **chromatog.** anal. software to identify and quantify peptide peaks and with data compilation programs to sort this information into spreadsheets for comparison of profiles among groups. The effects of postmortem delay or age were examd. by using rodent brain. Postmortem delay produced limited alterations to the profiles, but the effect of age was more pronounced. Many changes were apparent until 12 mo, after which the profiles became more const. Addnl. peptide profiling of the hippocampus demonstrated changes in peptide content as a function of perforant pathway ablation. The major strengths of HPLC-mediated peptide profiling are that it lends itself to automation and can be used to detect changes in peptides and small proteins among exptl. groups or subjects without any prior assumptions concerning which ones might be altered.

ST brain peptide protein profiling **chromatog** computer; HPLC peptide profiling brain; liq **chromatog** peptide profiling brain

IT Computer application
(in peptide profiling in brain of humans and lab. animals)

IT **Chromatography**, gel

(of peptides and small proteins, of brain of humans and lab. animals)
IT Development, mammalian
Senescence
(peptide profiles in brain in relation to)
IT Brain, composition
(peptides of, profiling of, **chromatog.** and computer methods for, in humans and lab. animals)
IT **Peptides, analysis**
RL: **ANST (Analytical study)**
(profiling of, of brain of humans and lab. animals, **chromatog.** and computer methods for)
IT **Chromatography**, column and liquid
(high-performance reversed-phase, of peptides and small proteins, of brain of humans and lab. animals)
IT **Chromatography**, column and liquid
(ion-exchange, of peptides and small proteins, of brain of humans and lab. animals)
IT **Proteins**, specific or class
RL: **ANST (Analytical study)**
(**low-mol.-wt.**, profiling of, of brain of humans and lab. animals, **chromatog.** and computer methods for)
IT Brain, disease
(perforant pathway, ablation, peptide profiles in brain response to, **chromatog.** in study of)

L40 ANSWER 8 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1991:578432 HCAPLUS
DN 115:178432
TI Quantitation of type I, III, and V collagens in human **tissue** samples by high-performance liquid **chromatography** of selected cyanogen bromide peptides
AU Miller, Edward J.; Furuto, Donald K.; Narkates, Annie J.
CS Dep. Biochem., Univ. Alabama, Birmingham, AL, 35294, USA
SO Anal. Biochem. (1991), 196(1), 54-60
CODEN: ANBCA2; ISSN: 0003-2697
DT Journal
LA English
CC **9-3** (Biochemical Methods)
Section cross-reference(s): 13
AB A method to det. the proportions of the major fiber-forming collagens (types I, III, and V) in noncartilaginous human **tissues** is presented. The procedure relies on direct solubilization of **tissue** collagen as CNBr peptides. The peptides are subjected to cation-exchange **chromatog.** followed by gel-permeation **chromatog.** in a manner consistent with the rapid resoln. and quantitation of relatively **low-mol.-wt.**
marker peptides for each collagen. The marker peptides utilized for type I, III, and V collagens are .alpha.I(I)-CB2, .alpha.1(III)-CB2, and .alpha.1(V)-CB1, resp. Quantitation of the peptides is attained as a function of UV absorbance during gel-permeation **chromatog.** The nature of the marker peptides, the use of HPLC techniques, and quantitation of the peptides by UV absorbance renders the method suitably rapid, sensitive, and accurate for routine evaluations of collagen compn. The utility of the method is illustrated in the presentation of analyses on specimens of placental membranes and blood vessel walls.
ST cation exchange HPLC collagen **tissue**; gel **chromatog** collagen animal **tissue**; liq **chromatog** collagen animal **tissue**
IT Placenta
(collagens detn. in human, by HPLC of selected cyanogen bromide peptides)
IT Blood vessel, composition
(collagens detn. in walls of human, by HPLC of selected cyanogen bromide peptides)
IT Organ
(collagens detn. in, of humans by HPLC of selected cyanogen bromide

peptides)
IT **Peptides, analysis**
RL: **ANT (Analyte); ANST (Analytical study)**
(detn. of, from cyanogen bromide cleavage of collagens, by HPLC)
IT Spectrochemical analysis
(UV, for peptides, for collagens detn. in human **tissues**)
IT Artery, composition
(aorta, collagens detn. in human, by HPLC of selected cyanogen bromide peptides)
IT Artery, composition
(coronary, left circumflex, collagens detn. in human, by HPLC of selected cyanogen bromide peptides)
IT **Chromatography**, gel
(high-performance, of peptides, for collagens detn. in human **tissue** samples)
IT **Chromatography**, column and liquid
(high-performance, cation-exchange, of peptides, for collagens detn. in human **tissue** samples)
IT Collagens, analysis
RL: ANT (Analyte); ANST (Analytical study)
(type I, detn. of, in human **tissue** samples by HPLC of selected cyanogen bromide peptides)
IT Collagens, analysis
RL: ANT (Analyte); ANST (Analytical study)
(type III, detn. of, in human **tissue** samples by HPLC of selected cyanogen bromide peptides)
IT Collagens, analysis
RL: ANT (Analyte); ANST (Analytical study)
(type V, detn. of, in human **tissue** samples by HPLC of selected cyanogen bromide peptides)
IT 136449-87-1
RL: ANST (Analytical study)
(as marker peptide, for collagen I detn. in human **tissue** samples)
IT 136431-31-7
RL: ANST (Analytical study)
(as marker peptide, for collagen III detn. in human **tissue** samples)
IT 136460-93-0, 147-200-Collagen (human type V .alpha.1-chain protein moiety)
RL: ANST (Analytical study)
(as marker peptide, for collagen V detn. in human **tissue** samples)
IT 506-68-3, Cyanogen bromide
RL: ANST (Analytical study)
(collagens cleavage by, peptides from, detn. of, by HPLC)

L40 ANSWER 9 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1990:213330 HCAPLUS
DN 112:213330
TI Use of gel filtration in the preparation of biological fluids for magnetic resonance spectroscopy
AU Hoffman, David W.; Venters, Ronald A.; Shedd, Suzanne F.; Spicer, Leonard D.
CS Med. Cent., Duke Univ., Durham, NC, 27710, USA
SO Magn. Reson. Med. (1990), 13(3), 507-13
CODEN: MRMEEN; ISSN: 0740-3194
DT Journal
LA English
CC **9-5** (Biochemical Methods)
AB Anal. of biol. fluids by proton magnetic resonance spectroscopy (MRS) is often complicated by dynamic range problems created from the large water resonance. Gel filtration **chromatog.** is found to be a simple and nondestructive method for exchanging D2O for H2O and for removing **low-mol.-wt.** mols. from both plasma and urine, significantly improving subsequent 1- and 2-dimensional MRS spectra.
ST gel **chromatog** biol fluid NMR **spectrometry**

IT **Body fluid**
(anal. of, by NMR **spectrometry**, after sample prepn. by gel filtration)
IT Blood analysis
Urine analysis
(by NMR **spectrometry**, after sample prepn. by gel filtration)
IT Lipoproteins
Amino acids, analysis
Carbohydrates and Sugars, analysis
Glycerides, analysis
Lipids, analysis
Phospholipids, analysis
Proteins, analysis
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(detection of, in blood plasma and urine by NMR **spectrometry** after sample purifn. by gel filtration)
IT Nuclear magnetic resonance **spectrometry**
(of biol. fluids, after sample prepn. by gel **chromatog.**)
IT **Chromatography**, gel
(of biol. fluids, for NMR spectrochem. anal.)
IT Spectrochemical analysis
(NMR, of biol. fluids, after sample prepn. by gel **chromatog.**)
IT 50-21-5, analysis 60-00-4, EDTA, analysis 60-00-4D, EDTA, metal complexes
RL: ANT (Analyte); ANST (Analytical study)
(detection of, in blood plasma and urine by NMR **spectrometry** after sample purifn. by gel filtration)

L40 ANSWER 10 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1987:152531 HCAPLUS
DN 106:152531
TI Fractionations of soluble proteins in human lenses with senile cataract by polyacrylamide gel electrophoresis
AU Kim, Bong Cheol; Choe, Joon Kiu
CS Sch. Med., Hanyang Univ., Seoul, S. Korea
SO Hanyang Uidae Haksulchi (1986), 6(2), 13-28
CODEN: HIHAD3
DT Journal
LA Korean
CC **9-15** (Biochemical Methods)
Section cross-reference(s): 14
AB To characterize the proteins and polypeptides in human lenses with senile cataract, sol. proteins in the cataractous lenses were isolated and fractionated by a DEAE-cellulose column **chromatog.**, native PAGE and SDS-PAGE, and the results were compared with those of normal human lenses. As compared with those in normal humans lenses, sol. protein contents were significantly decreased by 22% and insol. protein contents were markedly increased by approx. 3-fold in lenses with senile cataract. Sol. proteins in both normal and the cataractous lenses were sepd. into 7 peaks, resp. Protein peaks Vb and VII eluted in the cataractous lenses were not found in normal human lenses, suggesting that the 2 peaks may be responsible, in part, for pathogenesis of senile cataract. SDS-PAGE of the cataractous lens protein peaks revealed that protein peaks I, II, and III diminished in lenses with senile cataract were composed of **low mol. wt.** (LMW) polypeptides (15,00-28,000) and relatively large amts. of high mol. wt. (HMW) polypeptides (45,000 or above), and protein peaks Va and Vb increased in lenses with senile cataract were made up of LMW polypeptide (15,000-21,000) and relatively large amt. of HMW polypeptides. These results indicated that the LMW and HMW polypeptides in protein peaks I, II, and III appeared to be assocd. to form protein mols. in peak Va and Vb when normal human lenses were **transformed** into senile cataract. It could be suggested that these processes might play an important role in pathogenesis and maintenance of senile cataract. Protein and polypeptide bands sepd. by native-PAGE and SDS-PAGE appeared to be distinctive in normal lenses, but not distinctive and diffuse in the cataractous lenses. These results

indicated that, differing from those of normal lenses, polypeptides in the cataractous lenses were linked not only with the disulfide (SS) linkages, but also with non-SS, covalent linkages. Non-SS covalent changes in sol. protein mols. of lenses have been suggested to play a part in lens opacification.

ST sol protein eye lens fractionation; senile cataract protein PAGE; column **chromatog** protein cataract lens

IT **Chromatography**, column and liquid
(of sol. proteins, in human lenses with senile cataract)

IT **Proteins, analysis**
RL: **ANST (Analytical study)**
(sol., fractionation of, in human lenses with senile cataract by PAGE)

IT Electrophoresis and Ionophoresis
(gel, of sol. proteins, in human lenses with senile cataract, on polyacrylamide)

IT Eye, composition
(lens, sol. proteins in, fractionation of, by PAGE, of humans)

IT Cataract
(senile, sol. proteins in eye lenses of humans with)

L40 ANSWER 11 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1986:421315 HCAPLUS
DN 105:21315
TI Modified siliceous supports
IN Hou, Kenneth C.; Liao, Tung Ping D.
PA AMF Inc., USA
SO Eur. Pat. Appl., 75 pp.
CODEN: EPXXDW
DT Patent
LA English
IC ICM B01J020-32
ICS B01D015-04; B01J039-06
CC **9-3** (Biochemical Methods)
FAN.CNT 7

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 172579	A2	19860226	EP 1985-110571	19850822
	EP 172579	A3	19870107		
	EP 172579	B1	19921119		
	R: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
	US 4724207	A	19880209	US 1984-643613	19840822
	JP 61166861	A2	19860728	JP 1985-178490	19850813
	AT 82525	E	19921215	AT 1985-110571	19850822
PRAI	US 1984-643613	19840822			
	US 1983-466114	19830214			
	US 1984-576448	19840202			
	EP 1985-110571	19850822			

AB A modified silica material is described for the **chromatog**. sepn. and purifn. of biol. substances. The silica is covalently bonded to a synthetic polymer made from (a) a polymerizable compd. having a chem. group capable of covalent coupling with silica, and (b) .gtoreq.1 polymerizable compds. contg. an ionizable chem. group, a group capable of **transformation** to an ionizable chem. group, a group capable of covalent coupling to an affinity ligand or a biol. active mol., or a hydrophobic chem. group. For example, diethylaminoethylmethacrylate and glycidylmethacrylate were mixed in a closed reactor contg. H2O. N2 was bubbled to remove the air and an aq. mixt. of catalysts [(NH4)2S2O8, Na2S2O3] was added to the reactor. The reactor temp. was maintained at 40.degree. for 2 min. The excess catalyst and a **low-mol .-wt.** copolymer formed were added to silica particles. The pH of the reactor was reused to 9.0 and the temp. to 90.degree.-95.degree. for 1 h. The modified silica particles were filtered, washed, and returned to a reactor contg. MeC(:O)Et and H2O. 1,6-Dichlorohexane and kI were added to the reactor and the reaction mixt. was refluxed overnight. The resulting product was filtered, washed, and acidified with HCl to pH .apprx.5. This crosslinked, quaternized polymer bound to silica particles

had a 3-fold higher adsorption capacity for bovine serum albumin than silica prepd. with a silane coupling agent and 12-fold higher than untreated silica.

ST silica modified **chromatog** stationary phase; polymer linked silica **chromatog** support

IT Albumins, blood serum
RL: ANST (Analytical study)
(binding of, by polymer silica deriv., column **chromatog**. in relation to)

IT Kieselguhr
Mica-group minerals, compounds
Serpentine-group minerals
Silica gel, compounds
Smectite-group minerals
RL: SPN (Synthetic preparation); PREP (Preparation)
(polymer derivs., prepn. of, as stationary phases for column **chromatog**.)

IT Agglutinins and Lectins
Antibodies
Antigens
Carbohydrates and Sugars, compounds
Enzymes
Ligands
Nucleic acids
Proteins
RL: **ANST (Analytical study)**
(polymer silica deriv. bound to, as stationary phase for affinity **chromatog**.)

IT Pulp, cellulose
(polymer silica deriv. combined with, as stationary phase for column **chromatog**.)

IT Polymers, compounds
RL: SPN (Synthetic preparation); PREP (Preparation)
(silica derivs., prepn. of, as stationary phases for column **chromatog**.)

IT **Chromatography**, column and liquid
(stationary phases for, polymer silica derivs. as)

IT **Chromatography**, column and liquid
(affinity, stationary phases for, polymer silica derivs. as)

IT Glass, oxide
RL: SPN (Synthetic preparation); PREP (Preparation)
(porous, polymer derivs., prepn. of, as stationary phases for column **chromatog**.)

IT Globulins
RL: ANST (Analytical study)
(.gamma.-, binding of, by polymer silica deriv., column **chromatog**. in relation to)

IT 7440-70-2, biological studies
RL: BIOL (Biological study)
(binding of, by polymer silica deriv., column **chromatog**. in relation to)

IT 38742-80-2D, silica derivs.
RL: RCT (Reactant)
(crosslinking of, for stationary phases for column **chromatog**.)

IT 2163-00-0
RL: ANST (Analytical study)
(diethylaminoethyl methacrylate-glycidyl methacrylate copolymer crosslinking with)

IT 38742-80-2P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation)
(prepn. and reaction with silica)

IT 1318-00-9P 1318-74-7P, preparation 1318-93-0P, preparation 7631-86-9DP, polymer derivs. 12269-78-2P 14807-96-6DP, polymer derivs. 25067-05-4DP, silica derivs., sulfonylated
RL: SPN (Synthetic preparation); PREP (Preparation)

(prepn. of, as stationary phases for column **chromatog.**)

L40 ANSWER 12 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1985:484355 HCAPLUS
DN 103:84355
TI Fast protein liquid **chromatography** scale-up procedures for the preparation of **low-molecular-weight** proteins from urine
AU Cooper, E. H.; Turner, R.; Webb, J. R.; Lindblom, H.; Fagerstam, L.
CS Unit Cancer Res., Univ. Leeds, Leeds, LS2 9JT, UK
SO J. Chromatogr. (1985), 327, 269-77
CODEN: JOCRAM; ISSN: 0021-9673
DT Journal
LA English
CC **9-3** (Biochemical Methods)
AB A system for the rapid isolation of **low-mol.-wt.** proteins from urine has been devised, and illustrated by .alpha.1-microglobulin, .beta.2-microglobulin, retinol-binding protein, lysozyme, and monoclonal light chains. Urine proteins from patients with tubular dysfunction were concd., either by ultrafiltration or (NH4)2SO4 pptn. This was followed by gel **chromatog.** on Sephadex G 50. The appropriate fractions were then sepd. by **chromatog.** on Pharmacia monobead columns. A Mono Q strong anion exchanger was used for .beta.2-microglobulin, retinol-binding protein, .alpha.1-microglobulin, and free monoclonal light chains. Lysozyme was sepd. on a Mono S cation exchanger. The **chromatog.** was 1st optimized HR 5/5 columns and then scaled up to HR 16/10 columns.
ST protein liq **chromatog;** urine protein prepn
IT **Chromatography**, column and liquid
(fast, of **low-mol.-wt.** proteins of human urine, scale-up procedures for)
IT **Urine**
(**low-mol.-wt.** proteins purifn. from, of human by fast liq. **chromatog.**, scale-up procedures for)
IT **Chromatography**, gel
(of **low-mol.-wt.** proteins, from human urine)
IT **Chromatography**, column and liquid
(anion-exchange, of **low-mol.-wt.** proteins of human urine, scale-up procedures for)
IT **Chromatography**, column and liquid
(cation-exchange, of **low-mol.-wt.** proteins of human urine, scale-up procedures for)
IT **Proteins**
RL: **PUR (Purification or recovery)**; PREP (Preparation)
(**low-mol.-wt.**, purifn. of, from human urine by fast liq. **chromatog.**, scale-up procedures for)
IT Immunoglobulins
RL: PRP (Properties)
(monoclonal, light chains of, purifn. of, from human urine by fast liq. **chromatog.**, scale-up procedures for)
IT **Proteins**
RL: **PUR (Purification or recovery)**; PREP (Preparation)
(retinol-binding, purifn. of, from human urine by fast liq. **chromatog.**, scale-up procedures for)
IT Microglobulins
RL: PUR (Purification or recovery); PREP (Preparation)
(.alpha.1-, purifn. of, from human urine by fast liq. **chromatog.**, scale-up procedures for)
IT Microglobulins
RL: PUR (Purification or recovery); PREP (Preparation)
(.beta.2-, purifn. of, from human urine by fast liq. **chromatog.**, scale-up procedures for)
IT 9001-63-2P
RL: PUR (Purification or recovery); PREP (Preparation)
(purifn. of, from human urine by fast liq. **chromatog.**,

scale-up procedures for)

L40 ANSWER 13 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1983:194375 HCAPLUS
DN 98:194375
TI Reverse phase high-performance liquid **chromatography** for protein purification: insulin-like growth factors, calcium binding proteins and metallothioneins
AU Wilson, Kenneth J.; Berchtold, Martin W.; Zumstein, Peter; Klauser, Stephan; Hughes, Graham J.
CS Biochem. Inst., Univ. Zurich, Zurich, CH-8028, Switz.
SO Methods Protein Sequence Anal., [Proc. Int. Conf.], 4th (1982), Meeting Date 1981, 401-8. Editor(s): Elzinga, Marshall. Publisher: Humana, Clifton, N. J.
CODEN: 49KBAY
DT Conference
LA English
CC **9-3** (Biochemical Methods)
AB Human serum insulin-like growth factors, rat brain Ca2+-binding proteins, and rabbit liver metallothioneins were purified by microprocessor-controlled reversed-phase high-performance liq. **chromatog.** (HPLC) with UV detection, following preliminary purifn., including gel filtration. HPLC was carried out on LiChrosorb RP-18 or Aquapore RP 300 and elution was with a gradient formed between 0.1% H3PO4-10 mM NaClO4 (buffer A) and 60% MeCN (contg. 6% PrOH for Ca-binding proteins). For metallothionein purifn., the eluent was buffer A, Tris, pH 7.5, and 60% MeCN in buffer A. Two of the peaks in rat brain ext. were identified as calmodulin and parvalbumin and were shown to be homogeneous by 2-dimensional gel electrophoresis. The method allows the purifn. of relatively **low-mol.-wt.** proteins in active form.
ST protein purifn high performance **chromatog**; liq **chromatog** protein purifn; insulin like growth factor purifn; metallothionein purifn high performance **chromatog**; calcium binding protein metallothionein purifn; reversed phase **chromatog** protein purifn
IT Brain, composition
(calcium-binding proteins of, purifn. of, by reversed-phase high-performance liq. **chromatog.**)
IT Calmodulins
Parvalbumins
RL: ANT (Analyte); ANST (Analytical study)
(detection of, in calcium-binding proteins by reversed-phase high-performance liq. **chromatog.**)
IT **Blood**
(insulin-like growth factor of, purifn. of, of humans by reversed-phase high-performance liq. **chromatog.**)
IT Liver, composition
(metallothioneins of, purifn. of, by reversed-phase high-performance liq. **chromatog.**)
IT Metallothioneins
RL: PUR (Purification or recovery); PREP (Preparation)
(purifn. of, in liver by reversed-phase high-performance liq. **chromatog.**)
IT **Proteins**
RL: **PUR (Purification or recovery)**; PREP (Preparation)
(calcium-binding, purifn. of, in brain by reversed-phase high-performance liq. **chromatog.**)
IT **Chromatography**, column and liquid
(high-performance, reversed-phase, of proteins)
IT 61912-98-9P
RL: PUR (Purification or recovery); PREP (Preparation)
(purifn. of, in blood serum of humans by reversed-phase high-performance liq. **chromatog.**)

L40 ANSWER 14 OF 14 HCAPLUS COPYRIGHT 1999 ACS
AN 1979:553708 HCAPLUS

DN 91:153708
TI The application of gel filtration and specific analyses of urinary carbohydrate and protein material to the **diagnosis** of metabolic disorders
AU White, C. A.; Kennedy, J. F.
CS Inst. Ment. Subnorm., Lea Castle Hosp., Kidderminster/Worcs., DY10 3PP, Engl.
SO Clin. Chim. Acta (1979), 95(2), 381-9
CODEN: CCATAR; ISSN: 0009-8981
DT Journal
LA English
CC **9-2** (Biochemical Methods)
Section cross-reference(s): 14
AB A gel filtration method developed for urinary carbohydrate and proteinaceous material based on Bio-Gel P 2 cross-linked polyacrylamide gel has been coupled to specific continuous automated analyses for neutral and acidic carbohydrate and protein. The multichannel anal. system has been applied to urine from normal subjects and from known cases of genetic hyperglycosaminoglycanuria (mucopolysaccharidosis) to analyze not only the nondialyzable, high-mol.-wt. material but also the **low-mol.-wt.** material which comprises >90% of urine solutes in many cases. Urine from affected patients was easily distinguished from that from normal subjects and the method also differentiated between various syndromes. For the Morquio syndrome with mucopolysaccharidoria and Scheie syndrome, the ratio of acidic-to-neutral carbohydrate (carbazole-to-cysteine ratio) in the high-mol.-wt. material was the lowest (<0.6) whereas for the Hunter syndrome the value was >2.0, with values for Hunter and Sanfilippo syndromes being intermediate. The ratio of high-to-**low mol. wt.** material for the Morquio syndrome with mucopolysaccharidoria in the case of the borate-carbazole assay was lower (<0.2) but in the case of the L-cysteine-H2SO4 assay was higher (>0.6) than values obtained for the other syndromes. There was evidence for a division within the Sanfilippo syndrome using this mol. size ratio for the L-cysteine-H2SO4 assay, some with values >0.5 and some with values <0.3. In urine from cases of Morquio syndrome with mucopolysaccharidoria there was also evidence of large amts. of intermediate mol. wt. material. The application of this method to studies of other disorders of inherited metab. is equally possible and is discussed.
ST gel **chromatog** carbohydrate protein; urine carbohydrate protein detn; mucopolysaccharidosis urine carbohydrate protein; hyperglycosaminoglycanuria carbohydrate protein urine
IT Urine analysis
(carbohydrates and protein detn. in, by gel filtration in mucopolysaccharidosis)
IT Mucopolysaccharidosis
(carbohydrates and proteins detn. in urine in)
IT Carbohydrates, analysis
Proteins
RL: **ANT (Analyte); ANST (Analytical study)**
(detn. of, in urine by gel filtration in mucopolysaccharidosis)

=> d all tot l41

L41 ANSWER 1 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1999:484041 HCAPLUS
DN 131:267138
TI Application of a peptide bank from porcine brain in isolation of regulatory peptides
AU Seiler, Petra; Standker, Ludger; Mark, Silke; Hahn, Wilfried; **Forssmann, Wolf-Georg**; Meyer, Markus
CS Lower Saxony Institute for Peptide Research, Hannover, 30625, Germany
SO J. Chromatogr., A (1999), 852(1), 273-283
CODEN: JCRAEY; ISSN: 0021-9673
PB Elsevier Science B.V.
DT Journal

← applicants only

LA English
CC 2-1 (Mammalian Hormones)
Section cross-reference(s): **9**
AB Over the past years, the introduction of biol. assay systems, random peptide sequencing and orphan receptor screening has led to the isolation and identification of new regulatory peptides with potential clin. impact. We have developed a method for sepg. peptides into about 300 fractions from large amts. of porcine brain tissue. The prepn. of this peptide bank consists of three steps including ultrafiltration followed by cation-exchange sepn. and reversed-phase chromatog. These fractions represent the peptide bank with desalted and lyophilized peptides from brain tissue. Mol. masses of the peptides in the fractions are detd. by matrix-assisted laser desorption ionization MS and a mass data bank is subsequently generated. For systematic anal. of the peptides, a subsequent two-step purifn. procedure is followed by Edman sequencing resulting in the identification of different peptides. A survival assay with a neuronal cell line revealing the stimulatory and inhibitory activities is applied as a model to test the 300 fractions. This primary screen indicates that the biol. activities of the extd. peptides are easily characterized and, moreover, can be related to the biochem. entities. We conclude that the established peptide bank is an efficient and useful tool for the isolation of regulatory brain peptides applying different purifn. strategies.
ST peptide bank porcine brain regulatory peptide isolation
IT Brain
Swine
(application of a peptide bank from porcine brain in isolation of regulatory peptides)
IT **Peptides,** preparation
RL: **PUR (Purification or recovery);** PREP (Preparation)
(application of a peptide bank from porcine brain in isolation of regulatory peptides)
IT Matrix-assisted laser desorption ionization mass spectrometry
(for mol. mass detn.; prepn. of a peptide bank from porcine brain using ultrafiltration followed by cation-exchange sepn. and reversed-phase chromatog.)
IT Cation exchange
Reversed phase chromatography
Ultrafiltration
(prepn. of a peptide bank from porcine brain using ultrafiltration followed by cation-exchange sepn. and reversed-phase chromatog.)

L41 ANSWER 2 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1999:8785 HCAPLUS
DN 130:165123
TI Liquid **chromatography** and electrospray mass **spectrometric** mapping of peptides from human plasma filtrate
AU Raida, Manfred; **Schulz-Knappe, Peter;** Heine, Gabriele; **Forssmann, Wolf-Georg**
CS Lower Saxony Institute for Peptide Research, Hannover, D-30625, Germany
SO J. Am. Soc. Mass Spectrom. (1999), 10(1), 45-54
CODEN: JAMSEF; ISSN: 1044-0305
PB Elsevier Science Inc.
DT Journal
LA English
CC **9-16** (Biochemical Methods)
AB We present a multidimensional approach to map the compn. of complex peptide mixts. obtained as crude ext. from biol. liqs. by (1) cation exchange **chromatog.** and (2) subsequent microbore reversed-phase liq. **chromatog.** and electrospray mass **spectrometry** coupling (LC-MS). Human hemofiltrate is an equiv. to blood and is used to obtain peptide material in large quantities from patients with chronic renal failure. The upper exclusion limit of the filtration membranes used results in a protein-free filtrate contg. peptides in a range up to 20 ku. Using this unique peptide source, several thousand peptides were detected and an LC-MS data base of circulating human peptides was created. The

search for known peptides by their mol. mass is a reliable method to guide peptide purifn.
ST liq **chromatog** electrospray mass **spectrometric** mapping; peptide plasma
IT Reversed phase liquid **chromatography**
(Microbore; liq. **chromatog.** and electrospray mass **spectrometric** mapping of peptides from human plasma filtrate)
IT Cation exchange **chromatography**
Chronic renal failure
Electrospray ionization mass **spectrometry**
Liquid **chromatography**
Liquid **chromatography**-mass **spectrometry**
Membranes (nonbiological)
Purification
(liq. **chromatog.** and electrospray mass **spectrometric** mapping of peptides from human plasma filtrate)
IT **Peptides, analysis**
RL: **ANT (Analyte); ANST (Analytical study)**
(liq. **chromatog.** and electrospray mass **spectrometric** mapping of peptides from human plasma filtrate)
IT Mass
(molar; liq. **chromatog.** and electrospray mass **spectrometric** mapping of peptides from human plasma filtrate)

L41 ANSWER 3 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1998:597926 HCAPLUS
DN 129:341399
TI Peptide Trapping from human blood
AU **Schulz-Knappe, Peter**; Raida, Manfred; Hess, Rudiger; Kleemeier, Burkhard; Richter, Rudolf; **Schrader, Michael**; Standker, Ludger; **Forssmann, Wolf-Georg**
CS Lower Saxony Institute for Peptide Research (IPF), Hannover, D-30625, Germany
SO Pept. 1996, Proc. Eur. Pept. Symp., 24th (1998), Meeting Date 1996, 795-796. Editor(s): Ramage, Robert; Epton, Roger. Publisher: Mayflower Scientific, Kingswinford, UK.
CODEN: 66RCA5
DT Conference
LA English
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 14
AB Peptide Trapping is multidimensional peptide anal. that combines chromatog. methods, mass spectrometry, the systematic isolation and structural detn. of human peptides from blood. The Human Circulating Peptides Database is generated from the obtained data.
ST Peptide Trapping blood database; Human Circulating Peptides Database
IT Chromatography
Databases
Mass spectrometry
(peptide trapping from human blood)
IT Blood **proteins**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(peptide trapping from human blood)

L41 ANSWER 4 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1998:21559 HCAPLUS
DN 128:59181
TI Analysis of heart disease specific proteins using physical and chemical methods, especially HPLC and mass **spectrometry** for the direct diagnosis of point mutations caused by genetic or pathogenic factors.
IN **Forssmann, Wolf-Georg**; Raida, Manfred; Brenner, Bernhard; Nier, Volker
PA Forssmann, Wolf-Georg, Germany
SO Ger. Offen., 4 pp.
CODEN: GWXXBX

DT Patent
LA German
IC ICM C12Q001-24
ICS G01N030-72; G01N021-00
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 14
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI DE 19624802	A1	19980102	DE 1996-19624802	19960621
WO 9749993	A1	19971231	WO 1997-EP3241	19970620

W: JP, US
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

EP 914615	A1	19990512	EP 1997-929238	19970620

R: AT, CH, DE, FR, GB, IT, LI

PRAI DE 1996-19624802 19960621
WO 1997-EP3241 19970620

AB The invention concerns a quick medical diagnosis based on the quant. and qual. anal. of the proteins to detect exchanges of amino acids that demonstrate pathogenic or non-pathogenic effects on the organism. Proteins are isolated from biopsy samples, e.g. myosins from heart muscle, and are digested with endoproteinase, followed by sepn. of the peptides on a HPLC column. Fractions are identified either by a coupled mass **spectrometer** or the fractions are collected and analyzed subsequently by a MALDI mass **spectrometer** or by capillary electrophoresis. The comparison of protein samples of the healthy subjects and those of the ill ones offers a tool to identify mutations and to quantify changes from wild type to mutant.

ST diagnosis point mutation myosin heart disease; protein HPLC mass **spectrometry**

IT Capillary electrophoresis
Diagnosis
HPLC
Heart diseases
Liquid **chromatography**-mass **spectrometry**
Mass **spectrometry**
Matrix-assisted laser desorption ionization mass **spectrometry**
Point mutation
(anal. of heart disease specific proteins using phys. and chem. methods, esp. HPLC and mass **spectrometry** for direct diagnosis of point mutations caused by genetic or pathogenic factors)

IT Amino acids, analysis
Peptides, analysis
Proteins (general), **analysis**
RL: **ANT (Analyte)**; THU (Therapeutic use); **ANST (Analytical study)**; BIOL (Biological study); USES (Uses)
(anal. of heart disease specific proteins using phys. and chem. methods, esp. HPLC and mass **spectrometry** for direct diagnosis of point mutations caused by genetic or pathogenic factors)

IT .beta.-Myosins
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(.beta.-MHC; anal. of heart disease specific proteins using phys. and chem. methods, esp. HPLC and mass **spectrometry** for direct diagnosis of point mutations caused by genetic or pathogenic factors)

IT 9001-92-7, Endoproteinase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(anal. of heart disease specific proteins using phys. and chem. methods, esp. HPLC and mass **spectrometry** for direct diagnosis of point mutations caused by genetic or pathogenic factors)

L41 ANSWER 5 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1997:452608 HCAPLUS
DN 127:173432
TI Mapping of peptides and protein fragments in human urine using liquid **chromatography**-mass **spectrometry**

AU Heine, Gabriele; Raida, Manfred; **Forssmann, Wolf-Georg**
CS Lower Saxony Institute for Peptide Research, Feodor-Lynen-Strasse 31, Hannover, D-30625, Germany
SO J. Chromatogr., A (1997), 776(1), 117-124
CODEN: JCRAEY; ISSN: 0021-9673
PB Elsevier
DT Journal
LA English
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 2, 13, 80
AB A method for the mapping of peptide mixts., heterogeneous with respect to the concn. and the size of individual peptides, was established with the aim of obtaining a comprehensive anal. of human urine peptides. Peptide extn. and fractionation were optimized to achieve a 2-step anal., using reversed-phase and ion-exchange **chromatog.** Highly sensitive detection of peptides was performed by coupling microbore HPLC with electrospray mass **spectrometry** (ESI-MS). Peptides such as urodilatin, angiotensin, and fragments of psoriasin, granulin, and uromodulin were isolated and sequenced. The procedure presented here is a tool for the anal. of complex peptide mixts. from human urine.
ST urine peptide protein mapping HPLC **spectrometry**; liq **chromatog** peptide mapping urine; mass **spectrometry** peptide mapping urine; hormone peptide mapping urine GC MS
IT **Proteins** (specific **proteins** and subclasses)
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(granulins; peptides and protein fragments mapping in human urine by LC-MS)
IT Hormones (animal), analysis
RL: ANT (Analyte); ANST (Analytical study)
(peptide; peptides and protein fragments mapping in human urine by LC-MS)
IT Electrospray ionization mass **spectrometry**
Extraction
Ion exchange **chromatography**
Liquid **chromatography**-mass **spectrometry**
Protein sequence **analysis**
Reversed phase HPLC
Urine analysis
(peptides and protein fragments mapping in human urine by LC-MS)
IT **Peptides, analysis**
Proteins (general), **analysis**
Serum albumin
Tamm-Horsfall glycoprotein
.alpha.1-Microglobulins
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(peptides and protein fragments mapping in human urine by LC-MS)
IT **Proteins** (specific **proteins** and subclasses)
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(psoriasin; peptides and protein fragments mapping in human urine by LC-MS)
IT 9001-99-4, RNase
RL: ANT (Analyte); ANST (Analytical study)
(pancreatic; peptides and protein fragments mapping in human urine by LC-MS)
IT 1407-47-2, Angiotensin 115966-23-9, Urodilatin
RL: ANT (Analyte); ANST (Analytical study)
(peptides and protein fragments mapping in human urine by LC-MS)

L41 ANSWER 6 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1997:189925 HCAPLUS
DN 126:182307
TI Guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment
IN **Forssmann, Wolf-Georg**
PA Forssmann, Wolf-Georg, Germany
SO Ger. Offen., 15 pp.

CODEN: GWXXBX
DT Patent
LA German
IC ICM C07K014-435
ICS C12N015-11; C12N015-12; C12N015-63; C07K001-16; A61K038-17; A61K048-00
ICA G01N033-53; C12Q001-68
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 1, 2, **9**
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 19528544	A1	19970206	DE 1995-19528544	19950803
	WO 9706258	A2	19970220	WO 1996-EP3429	19960803
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9667892	A1	19970305	AU 1996-67892	19960803
PRAI	DE 1995-19528544		19950803		
	WO 1996-EP3429		19960803		

AB Guanylate cyclase-activating peptide II (GCAP-II); human cDNA for prepro-GCAP-II; method of purifying GCAP-II from human hemofiltrate or prepg. GCAP-II with recombinant cells; and use of GCAP-II or derivs. for treatment of gastrointestinal, urogenital, respiratory tract, cardiovascular, and nervous system diseases are disclosed. GCAP-II was purified from human hemofiltrate and its sequence was detd. The GCAP-II peptide was chem. synthesized and tested for biol. activity. The cDNA for human prepro-GCAP-II was cloned and sequenced.

ST sequence guanylate cyclase activating peptide cDNA
IT Urogenital tract
(diseases; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT cDNA sequences
(for prepro-guanylate cyclase-activating peptide II of human)
IT Cardiovascular diseases
Digestive system diseases
Gene therapy
Nervous system diseases
Respiratory tract diseases
(guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT Probes (nucleic acid)
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT **Protein** sequences
(of prepro-guanylate cyclase-activating peptide II of human)
IT Livestock
(transgenic; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT 187224-17-5 187224-19-7 187224-21-1, 2-16-Uroguanylin (human reduced) 187224-23-3, 3-16-Uroguanylin (human) 187224-24-4 187224-26-6, 4-16-Uroguanylin (human reduced) 187224-27-7, 6-16-Uroguanylin (human reduced)
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(GCAP-II peptide; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT 173833-60-8
RL: PRP (Properties)
(amino acid sequence; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)
IT 187286-48-2 187286-49-3 187286-50-6 187286-51-7

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)

IT 170245-20-2P, Guanylate cyclase-activating peptide II (human reduced)
RL: PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)

IT 168658-36-4, GenBank Z50753
RL: PRP (Properties)
(nucleotide sequence; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)

IT 187224-25-5 187285-49-0 187285-50-3 187413-32-7 187413-34-9
187413-40-7 187413-42-9 187413-44-1 187413-45-2 187413-47-4
187413-48-5 187413-49-6
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(prepro-GCAP-II peptide; guanylate cyclase-activating peptide II, cDNA for GCAP-II, and use of GCAP-II and nucleic acid for disease diagnosis and treatment)

L41 ANSWER 7 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:639463 HCAPLUS
DN 125:322258
TI Isolation of peptides from human hemofiltrate: Strategy of systematic characterization
AU **Schulz-Knappe, P.**; Bensch, K. W.; Schepky, A. G.; Hess, R.; Staendker, L.; Heine, G.; Sillard, R.; Raida, M.; **Forssmann, W. -G.**
CS Lower Saxony Institute Peptide Research, Hannover, D-30625, Germany
SO Pept. 1994, Proc. Eur. Pept. Symp., 23rd (1995), Meeting Date 1994, 433-434. Editor(s): Maia, Hernani L. S. Publisher: ESCOM, Leiden, Neth. CODEN: 63MBAO
DT Conference
LA English
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 2
AB The authors isolated and systematically characterized circulating human peptides in 5000 dm3 of human hemofiltrate by cation-exchange extn., salt pptn., ultrafiltration, preparative cation-exchange **chromatog.**, and HPLC-mass **spectrometry**. Some 15 peptides in a peptide-contg. fraction were detected and characterized. This systematic anal. of human circulating peptides provides new information on known peptides and is an effective tool to detect new circulating peptides. Advantages of the HPLC-mass **spectrometry** method are discussed.
ST peptide isolation hemofiltrate liq **chromatog spectrometry**; mass **spectrometry** peptide blood filtrate
IT Extraction
(cation-exchange; peptides systematic characterization in human hemofiltrate)
IT Blood analysis
Mass **spectrometry**
Precipitation
(peptides systematic characterization in human hemofiltrate)
IT **Peptides, analysis**
RL: **ANT (Analyte); PUR (Purification or recovery); ANST (Analytical study)**; PREP (Preparation)
(peptides systematic characterization in human hemofiltrate)
IT **Chromatography**, column and liquid
(high-performance, peptides systematic characterization in human hemofiltrate)
IT **Chromatography**, column and liquid
(preparative, cation-exchange; peptides systematic characterization in

human hemofiltrate)
IT Filtration
(ultra-, of blood, peptides systematic characterization in human hemofiltrate)

L41 ANSWER 8 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:639454 HCAPLUS
DN 125:322134
TI Determination of sulfated peptides in human hemofiltrate by differential iodination
AU Schepky, A. G.; **Schulz-Knappe, P.; Forssmann, W. -G.**
CS Lower Saxony Institute Peptide Research, Hannover, D-30625, Germany
SO Pept. 1994, Proc. Eur. Pept. Symp., 23rd (1995), Meeting Date 1994, 412-413. Editor(s): Maia, Hernani L. S. Publisher: ESCOM, Leiden, Neth. CODEN: 63MBAO
DT Conference
LA English
CC **9-8** (Biochemical Methods)
AB A method is presented to facilitate the detection and subsequent quantification of sulfated peptides in crude biol. mixts., e.g., human hemofiltrate. After peptide extn. by preparative anion-exchange **chromatog.**, a concd. mixt. of peptides was obtained. The degree of radioiodination without previous desulfation was detd. to obtain control values, and then the sequence of cold iodination, desulfation, and radioiodination was applied. The data acquired was submitted to subtractive anal., thus reducing the background of radioiodination due to incomplete satn. of iodine-binding sites.
ST hemofiltrate sulfated peptide detn differential iodination; radioiodination tyrosine sulfate detn peptide blood; blood filtrate sulfated peptide detn
IT Blood analysis
Iodination
(sulfated peptides detn. in human hemofiltrate by differential iodination)
IT **Peptides, analysis**
RL: **ANT (Analyte); ANST (Analytical study)**
(sulfated; sulfated peptides detn. in human hemofiltrate by differential iodination)
IT Iodination
(radiochem., sulfated peptides detn. in human hemofiltrate by differential iodination)
IT Filtration
(ultra-, of blood, sulfated peptides detn. in human hemofiltrate by differential iodination)
IT 956-46-7, Tyrosine sulfate
RL: ANT (Analyte); ANST (Analytical study)
(of blood, sulfated peptides detn. in human hemofiltrate by differential iodination)

L41 ANSWER 9 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:551840 HCAPLUS
DN 125:269683
TI Specific determination of tyrosine-phosphorylated proteins and peptides by differential iodination
AU Schepky, Andreas G.; Meinhardt, Gerold; Austermann, Sabine; Adermann, Knut; **Schulz-Knappe, Peter; Forssmann, Wolf-Georg;** Hass, Ralf
CS Niedersaechsisches Institut fuer Peptid-Forschung GmbH, Feodor Lynen Str. 31, D-30625, Hannover, Germany
SO J. Chromatogr., A (1996), 743(2), 273-282 CODEN: JCRAEY; ISSN: 0021-9673
DT Journal
LA English
CC **9-8** (Biochemical Methods)
AB A new method for the selective and quant. detn. of phosphotyrosine residues is presented using a differential iodination technique.

Characterization of tyrosine-phosphorylated proteins was performed in a biol. system using human U937 myeloid leukemia cells. The method is based on the satn. of free iodine binding sites using nonradioactive iodine. Samples are then treated with alk. phosphatase. New iodine binding sites in dephosphorylated tyrosines are subsequently radioiodinated, resulting in specific labeling of tyrosine phosphates. Sepn. is performed by RP-HPLC or SDS-PAGE. Radiolabeled proteins are then identified using a radioactivity detector or autoradiog.

ST tyrosine phosphorylated protein peptide detn radiometry

IT **Peptides, analysis**
Proteins, analysis
RL: **ANT (Analyte); ANST (Analytical study)**
(tyrosine-phosphorylated; specific radiometric detn. of tyrosine-phosphorylated proteins and peptides by differential iodination)

IT Animal cell line
(U937, specific radiometric detn. of tyrosine-phosphorylated proteins and peptides by differential iodination)

IT 21820-51-9, Phospho-L-tyrosine
RL: ANT (Analyte); ANST (Analytical study)
(specific radiometric detn. of tyrosine-phosphorylated proteins and peptides by differential iodination)

L41 ANSWER 10 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:438376 HCAPLUS
DN 125:136673
TI Systematic isolation of circulating human peptides: The concept of peptide trapping
AU **Schulz-Knappe, P.**; Raida, M.; Meyer, M.; Quellhorst, E. A.; **Forssmann, W. -G.**
CS Lower Saxony Institute Peptide Research, Hannover, Germany
SO Eur. J. Med. Res. (1996), 1(5), 223-236
CODEN: EJMRFL; ISSN: 0949-2321
DT Journal; General Review
LA English
CC **9-0** (Biochemical Methods)
AB A review with 66 refs. The structural detn. of circulating human peptides is essential to det. their correct posttranslationally processed form. Human hemofiltrate from patients with end stage renal disease is accessible in large quantities and is used as a source for the prepn. of circulating peptides. After complete peptide extn. from hemofiltrate, a systematic sepn. with different **chromatog.** techniques is achieved. Single peptides are selected according to their mass and **chromatog.** elution position. Following **chromatog.** purifn., amino acid sequence anal. is performed in combination with data base search. The identification of circulating peptides leads to numerous fragments resulting from cleavage of larger plasma proteins as well as to the discovery of new peptide hormones. The results obtained so far give insight into the degrdn. of plasma proteins such as fibrinogen, which results in the generation of fragments with biol. activity themselves and in the identification of a novel cytokine HCC-1, the first member of .beta.-defensins in humans, hBD-1, and different peptides not present in any data base.

ST review systematic isolation circulating peptide trapping

IT **Peptides**, preparation
RL: **PUR (Purification or recovery)**; PREP (Preparation)
(circulating; systematic isolation of circulating human peptides)

L41 ANSWER 11 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1996:200169 HCAPLUS
DN 124:255247
TI Human circulating .beta.-defensin hBD-1
IN Bensch, Klaus W.; **Forssmann, Wolf-Georg**; **Schulz-Knappe, Peter**
PA Germany
SO Ger. Offen., 13 pp.

CODEN: GWXXBX
DT Patent
LA German
IC ICM C07K007-00
ICS A61K038-22; A61K049-00
CC **9-5** (Biochemical Methods)
Section cross-reference(s): 3, 13
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI DE 4427531	A1	19960208	DE 1994-4427531	19940804

AB An antibiotic peptide, hBD-1, is isolated from human hemofiltrate and a cDNA is provided for prodn. of recombinant hBD-1 for diagnosis and treatment of disturbances in inflammatory and immune processes. Thus, hBD-1, with 36 amino acid residues, was purified from human hemofiltrate by (NH4)2SO4 pptn., ultrafiltration, and chromatog. and sequenced. Degenerate PCR primers based on this sequence were synthesized and used to amplify hBD-1 cDNA from various human tissues; the cDNA was also sequenced.

ST defensin purifn sequence cDNA; antibiotic peptide blood defensin
IT Inflammation
(disorder, diagnosis of; human circulating .beta.-defensin hBD-1)
IT Ribonucleic acids, messenger
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(for .beta.-defensin, in diagnosis of inflammatory and immune disorders)
IT Gene, animal
RL: BOC (Biological occurrence); BPR (Biological process); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(for .beta.-defensin; human circulating .beta.-defensin hBD-1)
IT Antibiotics
Deoxyribonucleic acid sequences
Inflammation inhibitors
Protein sequences
(human circulating .beta.-defensin hBD-1)
IT Macrophage
(migration disorder, .beta.-defensin for treatment of)
IT Diagnosis
(of inflammatory and immune disorders; human circulating .beta.-defensin hBD-1)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(to .beta.-defensin, in diagnosis of inflammatory and immune disorders)
IT Blood analysis
(.beta.-defensin detn. in)
IT Cerebrospinal fluid
Urine analysis
(.beta.-defensin detn. in, in diagnosis of inflammatory and immune disorders)
IT Blood
(.beta.-defensin purifn. from human)
IT Immunity
(disorder, diagnosis of; human circulating .beta.-defensin hBD-1)
IT Antibodies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(monoclonal, to .beta.-defensin, in diagnosis of inflammatory and immune disorders)
IT 167679-93-8P
RL: BOC (Biological occurrence); PRP (Properties); PUR (Purification or recovery); SPN (Synthetic preparation); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(human circulating .beta.-defensin hBD-1)
IT 174957-49-4P 174957-80-3P
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(human circulating .beta.-defensin hBD-1)

L41 ANSWER 12 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1995:398249 HCAPLUS
DN 122:182324
TI High-performance liquid **chromatographic** determination of sulfated peptides in human hemofiltrate using a radioactivity monitor
AU Schepky, Andreas G.; **Schulz-Knappe, Peter**; **Forssmann, Wolf-Georg**
CS Niedersaechsisches Institut fuer Peptid-Forschung GmbH, Feodor-Lynen-Strasse 31, Hannover, 30625, Germany
SO J. Chromatogr., A (1995), 691(1-2), 255-61
CODEN: JCRAEY
DT Journal
LA English
CC **9-3** (Biochemical Methods)
AB Specific labeling of tyrosine sulfate-contg. peptides was achieved using a differential iodination approach. In a complex peptide mixt. from human hemofiltrate, cold iodination to sat. free iodine binding sites was followed by mild acidic desulfation of tyrosine sulfate and subsequent radioiodination using iodine-125. Reaction steps were controlled by amino acid anal. using o-phthaldialdehyde precolumn derivatization and by spiking with a sulfated cholecystokinin fragment (CCK4-S). Sepn. of the peptide mixt. with RP-HPLC on a C18 column coupled to a radioactivity monitor led to the sensitive (.ltoreq.5 pM) and specific detn. of tyrosine sulfate-contg. peptides.
ST liq **chromatog** sulfated peptide hemofiltrate
IT **Peptides, analysis**
RL: **ANT (Analyte)**; **ANST (Analytical study)**
(sulfated; high-performance liq. **chromatog**. detn. of sulfated peptides in human hemofiltrate using a radioactivity monitor)
IT **Chromatography**, column and liquid
(high-performance, high-performance liq. **chromatog**. detn. of sulfated peptides in human hemofiltrate using a radioactivity monitor)

L41 ANSWER 13 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1995:234752 HCAPLUS
DN 122:24582
TI Purification and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use
IN **Forssmann, Wolf Georg**; Hill, Oliver; Zucht, Hans Dieter; Kuhn, Michaela; Maegert, Hans Juergen; Adermann, Knut; Raida, Manfred; **Schulz-Knappe, Peter**
PA Forssmann, Wolf Georg, Germany
SO Ger. Offen., 27 pp.
CODEN: GWXXBX
DT Patent
LA German
IC ICM C07K007-10
ICS C07K003-20; A61K037-02
ICA C12N009-88; C12N015-79; C12N015-74; C12N015-70
CC 2-6 (Mammalian Hormones)
Section cross-reference(s): 1, **9**
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI DE 4309815	A1	19940929	DE 1993-4309815	19930326

AB The GAP-1 guanylate cyclase-activating peptide that plays a role in hormonal processes in the digestive tract is purified from human blood. The protein is useful in the diagnosis and treatment of digestive tract disorders. The peptide was purified from a hemo-filtrate prepd. with a 20,000 Da-cutoff filter using seven chromatog. steps with activity monitored by a bioassay using T84 cells. Chem. synthesis of the peptide and of active fragments is demonstrated.
ST guanylate cyclase activating peptide serum purifn; GAP1 serum purifn synthesis
IT **Protein** sequences

(of guanylate cyclase activating peptide GAP-1 of human)
IT Blood
(purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)
IT Antibodies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(to guanylate cyclase-activating peptide GAP-1 of human; purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)
IT Heart, disease
Kidney, disease
Lung, disease
(treatment of; purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)
IT Digestive tract
Genitourinary tract
Nervous system
(disease, treatment of; purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)
IT **Proteins**, specific or class
RL: BSU (Biological study, unclassified); **PUR (Purification or recovery)**; SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(guanylate cyclase-activating, GAP-1; purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)
IT 150295-38-8P 150549-36-3P, Guanylin, pro- (human clone pHPG2) 159544-22-6P 159544-23-7P
RL: BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; purifn. and synthesis of a guanylate cyclase-activating peptide (GAP-1) from human blood for therapeutic use)

L41 ANSWER 14 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1994:318508 HCAPLUS
DN 120:318508
TI Human hemofiltrate as a source of circulating bioactive peptides: determination of amino acids, peptides and proteins
AU Schepky, Andreas G.; Bensch, Klaus W.; **Schulz-Knappe, Peter**; **Forssmann, Wolf Georg**
CS Niedersaechs. Inst. Pept.-Forsch. GmbH, Hannover, 30625, Germany
SO Biomed. Chromatogr. (1994), 8(2), 90-94
CODEN: BICHE2; ISSN: 0269-3879
DT Journal
LA English
CC **9-3** (Biochemical Methods)
Section cross-reference(s): 14
AB Human hemofiltrate (HF) was evaluated regarding its content of free amino acids, proteins, and regulatory peptides. Human HF was obtained from patients with end stage renal disease (ESRD). In contrast to plasma it mainly contains low and middle wt. mols. <45 kDa. The content of free amino acids, peptides, and proteins in pooled filtrate was detd. by amino acid anal. using ortho-phthaldialdehyde/fluorenyl Me chloroformate precolumn derivatization. The total amt. of peptides and proteins in human HF is 49.4 mg/L. The levels of all free amino acids (230 mg/L) and the concn. of some regulatory peptides like insulin, endothelin, gastrin, vasopressin and angiotensin II were similar compared with blood plasma. The amt. of peptides and proteins detected in the filtrate was around 0.07% of total plasma proteins and consisted mainly of smaller proteins and peptides as shown by size exclusion **chromatog.** The presence of large proteins in plasma is reduced by a factor of 1500 after filtration. The authors conclude that human hemofiltrate is a valuable source for the large-scale extn. of regulatory peptides.

ST hemofiltrate amino acid peptide protein detn; blood dialysis filtrate peptide detn; **chromatog** hemofiltrate analysis
IT Amino acids, analysis
Peptides, analysis
Proteins, analysis
RL: **ANT (Analyte); ANST (Analytical study)**
(detn. of, in human hemofiltrate, blood plasma compn. in relation to)
IT Kidney, disease
(failure, amino acids and peptides and proteins detn. in dialysis hemofiltrate from, blood plasma compn. in relation to)
IT Dialysis
(hemo-, amino acids and peptides and proteins detn. in filtrate from, in human)
IT 56-40-6, Glycine, analysis 56-41-7, Alanine, analysis 56-45-1, Serine, analysis 56-84-8, Aspartic acid, analysis 56-85-9, Glutamine, analysis 56-86-0, Glutamic acid, analysis 56-87-1, Lysine, analysis 60-18-4, Tyrosine, analysis 61-90-5, Leucine, analysis 63-68-3, Methionine, analysis 63-91-2, Phenylalanine, analysis 70-47-3, Asparagine, analysis 71-00-1, Histidine, analysis 72-18-4, Valine, analysis 72-19-5, Threonine, analysis 73-22-3, Tryptophan, analysis 73-32-5, Isoleucine, analysis 74-79-3, Arginine, analysis 147-85-3, Proline, analysis 9002-76-0, Gastrin 9004-10-8, Insulin, analysis 11000-17-2, Vasopressin 11128-99-7, Angiotensin II 116243-73-3, Endothelin
RL: ANT (Analyte); ANST (Analytical study)
(detn. of, in human hemofiltrate, blood plasma compn. in relation to)

L41 ANSWER 15 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1994:293504 HCAPLUS
DN 120:293504
TI Determination of sulfated peptides by differential iodination
AU Schepky, Andreas G.; Schmidt, Andre M.; Schmidt, Thomas; **Schulz-Knappe, Peter; Forssmann, Wolf Georg**
CS Niedersaechsisches Inst., Peptid-Forschung GmbH, Hannover, D-30625, Germany
SO Biol. Chem. Hoppe-Seyler (1994), 375(3), 201-3
CODEN: BCHSEI; ISSN: 0177-3593
DT Journal
LA English
CC **9-16** (Biochemical Methods)
Section cross-reference(s): 2
AB A sequential approach was developed to label tyrosine sulfate and peptides contg. tyrosine sulfate selectively. Amino acids and peptides contg. tyrosine and tyrosine sulfate were first iodinated using the chloramine-T method. Reaction products were detd. by RP-HPLC. Mono- and diiodination of tyrosine and several model peptides was achieved within 120 s incubation time. Iodination of free tyrosine sulfate and sulfated cholecystokinin26-33 was <5%. After desulfation of the reaction products with 1N HCl, successful radioiodination of desulfated tyrosine was carried out whereas tyrosine incorporated radioactive iodine only 10%. As shown by RP-HPLC specific labeling of tyrosine sulfate-contg. peptides with 125I was achieved.
ST sulfated peptide detn differential iodination
IT Iodination
(sulfated peptides detn. by differential)
IT **Peptides**, reactions
RL: RCT (Reactant)
(tyrosine sulfate-contg., iodination of, detn. in relation to)
IT **Peptides**, reactions
RL: RCT (Reactant)
(tyrosine-contg., iodination of, detn. in relation to)
IT **Peptides**, compounds
RL: **ANT (Analyte); ANST (Analytical study)**
(tyrosine-contg., sulfated, detn. of, by differential iodination)
IT 60-18-4, Tyrosine, reactions 60-18-4D, Tyrosine, peptides contg. 956-46-7, Tyrosine sulfate 956-46-7D, Tyrosine sulfate, peptides contg. 25126-32-3 25679-24-7 155070-90-9

RL: RCT (Reactant)
(iodination of, sulfated peptides detn. in relation to)
IT 7553-56-2
RL: ANST (Analytical study)
(iodination, sulfated peptides detn. by differential)

L41 ANSWER 16 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1993:665548 HCAPLUS
DN 119:265548
TI Immunochemistry of peptide. II. Immunohistochemical studies using antibodies against synthetic peptides
AU Mifune, Hiroharu; Nokihara, Kiyoshi; Suzuki, Syusaku; **Forssmann, Wolf Georg**
CS Sch. Med., Kurume Univ., Kurume, 830, Japan
SO Shimadzu Hyoron (1993), 50(1), 129-36
CODEN: SHHYAG; ISSN: 0371-005X
DT Journal; General Review
LA Japanese
CC **9-0** (Biochemical Methods)
Section cross-reference(s): 2, 15
AB A review with 17 refs. on immunohistochem. studies using antibodies against synthetic peptides. Progress in immunohistochem. and fundamental histochem. methods using specific antibodies against synthetic peptides are described in detail. The previous immunohistochem. studies on cardiodilatin, a cardiac hormone, are also described.
ST immunohistochem peptide antibody review
IT Antibodies
RL: ANST (Analytical study)
(in peptide immunohistochem. study)
IT **Peptides**, biological studies
RL: BIOL (Biological study)
(synthetic, immunohistochem. of, antibodies in study of)
IT Immunoassay
(immunohistochem., of peptides, antibodies in study of)
IT 92047-08-0, Cardiodilatin
RL: PROC (Process)
(immunohistochem. study of, antibodies in)

L41 ANSWER 17 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1988:401491 HCAPLUS
DN 109:1491
TI Recovery of biologically active proteins and peptides from hemodialyzate, hemofiltrate, or body fluids
IN **Forssmann, Wolf Georg**
PA Fed. Rep. Ger.
SO Ger. Offen., 3 pp.
CODEN: GWXXBX
DT Patent
LA German
IC ICM C07K015-06
ICS C07K007-40; C07K007-34; C07K007-32; C07K007-30; C07K003-02
ICA C07K003-28
CC 2-1 (Mammalian Hormones)
Section cross-reference(s): **9**, 63
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 3633797	A1	19880407	DE 1986-3633797	19861003
	DE 3633797	C2	19950810		

AB The liq. produced as a byproduct during hemodialysis or hemofiltration, contg. blood proteins and peptides of mol. wt. <20,000, is used for recovery of biol. active proteins and peptides, e.g. insulin and other peptide hormones. Protein-contg. hemofiltrate was adjusted to pH 2.7 with AcOH and mineral acid, and 2.5 kg alginic acid/1000 L was added with stirring. After 10 h, the alginic acid with bound peptides was filtered out and washed with EtOH and 0.05M mineral acid. After addn. of 0.2M

mineral acid, the peptides were concd. in <5 L and salted out with satd. NaCl at pH 3.8-4.0. The peptides were further purified by gel filtration or ultrafiltration followed by lyophilization. The product contained cardiodilatin 99-126, insulin, glucagon, secretin, gastrin, etc. as shown by RIA, bioassay.

ST proteïn recovery hemodialyzate hemofiltrate; peptide recovery hemodialyzate hemofiltrate

IT Adsorbents
(for peptide and protein recovery from hemodialyzate or hemofiltrate)

IT **Peptides**, biological studies
RL: BIOL (Biological study)
(hormones, recovery of, from hemodialyzate or hemofiltrate)

IT Heart, composition
(peptide hormones of, recovery of, from hemodialyzate or hemofiltrate)

IT Silica gel, biological studies
RL: BIOL (Biological study)
(peptides and proteins recovery from hemodialyzate or hemofiltrate by adsorption on)

IT Ascitic fluid
Cerebrospinal fluid
Urine
(peptides and proteins sepn. from)

IT Hormones
RL: BIOL (Biological study)
(peptides, recovery of, from hemodialyzate or hemofiltrate)

IT Gastrointestinal hormones
Neurohormones
Pituitary hormones
Thyroid hormones
Proteins, preparation
RL: PROC (Process)
(recovery of, from hemodialyzate or hemofiltrate)

IT Dialysis
(hemo-, peptides and proteins recovery from waste liq. from)

IT Filtration
(ultra-, of blood, peptides and proteins recovery from waste liq. from)

IT 1343-98-2P, Silicic acid 9005-32-7P, Alginic acid
RL: PREP (Preparation)
(peptides and proteins recovery from hemodialyzate or hemofiltrate by adsorption on)

IT 9007-92-5P, Glucagon, biological studies 52906-92-0P, Motilin 107852-16-4P, Cadiodilatin-28
RL: BIOL (Biological study); PREP (Preparation)
(recovery of, from hemodialyzate or hemofiltrate)

IT 1393-25-5P, Secretin 9002-64-6P, Parathyroid hormone 9002-76-0P, Gastrin 9004-10-8P, Insulin, biological studies
RL: PREP (Preparation)
(recovery of, from hemodialyzate or hemofiltrate)

L41 ANSWER 18 OF 18 HCAPLUS COPYRIGHT 1999 ACS
AN 1983:157423 HCAPLUS
DN 98:157423
TI Region-specific radioimmunoassay and its application to the study of neurotensin-related peptides in the chicken
AU Carraway, Robert E.; Reinecke, M.; **Forssmann, W. G.**
CS Med. Sch., Univ. Massachusetts, Worcester, MA, USA
SO Pharmacol. Biochem. Aspects Neurotransm. Recept., Taniguchi Symp. Brain Sci., 4th (1983), Meeting Date 1980, 205-25. Editor(s): Yoshida, Hiroshi; Yamamura, Henry I. Publisher: Wiley, New York, N. Y.
CODEN: 49LKAW
DT Conference
LA English
CC **9-10** (Biochemical Methods)
Section cross-reference(s): 12
AB A general method which uses RIA and gel **chromatog.** for the detection and isolation of variants of known peptides is outlined and

discussed. The method was used to characterize immunochem. the neurotensin family in vertebrates and to isolate and identify neurotensin-related peptides in chicken.
ST chicken neurotensin peptide radioimmunoassay; gel **chromatog** peptide
IT Chicken
(neurotensin-related peptides detn. in, by region-specific radioimmunoassay)
IT **Peptides, analysis**
RL: **ANST (Analytical study)**
(neurotensin-related, detn. of, in chicken by region-specific radioimmunoassay)
IT **Chromatography**, gel
(of peptides)
IT Immunochemical analysis
(radioimmunoassay, region-specific, for neurotensin-related peptides)
IT 39379-15-2
RL: ANST (Analytical study)
(peptides related to, detn. of, in chicken by region-specific radioimmunoassay)

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L42 544 S E14,E15,E25-E32
E SCHULZ KNAP/AU
L43 55 S E4-E6
E SCHRADER M/AU
L44 106 S E3-E9,E18,E19
E OPITZ H/AU
L45 93 S E3,E4,E9
L46 738 S L42-L45
L47 387 S L46 AND (10054 OR 10064)/CC
L48 293 S L46 AND (PEPTIDE OR PROTEIN)
L49 479 S L47,L48
L50 8 S L49 AND MOLECULAR WEIGHT
L51 47 S L49 AND (?CHROMATOG? OR ?SPECTROM?)
L52 31 S L51 AND (10050 OR 10504)/CC
L53 24 S L51 AND (*10050 OR *10504)/CC
L54 4 S L53 AND DATA?
L55 2 S L54 NOT (SLURP OR BITISTATIN)/TI
L56 4 S (MAPPING OR BANK)/TI AND L51
L57 5 S L55,L56

=> d all tot l57

L57 ANSWER 1 OF 5 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:396359 BIOSIS
DN PREV199900396359

TI Application of a **peptide bank** from porcine brain in isolation of regulatory **peptides**.
AU Seiler, Petra; Staendker, Ludger; Mark, Silke; Hahn, Wilfried; **Forssmann, Wolf-Georg**; Meyer, Markus (1)
CS (1) Lower Saxony Institute for Peptide Research, Feodor-Lynen-Strasse 31, 30625, Hannover Germany
SO Journal of Chromatography A, (Aug. 6, 1999) Vol. 852, No. 1, pp. 273-283. ISSN: 0021-9673.
DT Article
LA English
SL English
AB Over the past years, the introduction of biological assay systems, random **peptide** sequencing and orphan receptor screening has led to the isolation and identification of new regulatory **peptides** with potential clinical impact. We have developed a method for separating **peptides** into about 300 fractions from large amounts of porcine brain tissue. The preparation of this **peptide** bank consists of three steps including ultrafiltration followed by cation-exchange separation and reversed-phase **chromatography**. These fractions represent the **peptide** bank with desalted and lyophilized **peptides** from brain tissue. Molecular masses of the **peptides** in the fractions are determined by matrix-assisted laser desorption ionization MS and a mass **data** bank is subsequently generated. For systematic analysis of the **peptides**, a subsequent two-step purification procedure is followed by Edman sequencing resulting in the identification of different **peptides**. A survival assay with a neuronal cell line revealing thestimulatory and inhibitory activities is applied as a model to test the 300 fractions. This primary screen indicates that the biological activities of the extracted **peptides** are easily characterized and, moreover, can be related to the biochemical entities. We conclude that the established **peptide** bank is an efficient and useful tool for the isolation of regulatory brain **peptides** applying different purification strategies.
CC Biochemical Studies - General *10060
Biochemical Methods - General *10050
Biophysics - General Biophysical Studies *10502
Nervous System - General; Methods *20501
BC Suidae 85740
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Parts, Structures, & Systems of Organisms
brain: nervous system
IT Chemicals & Biochemicals
regulatory **peptides**: analysis, isolation
IT Methods & Equipment
cation-exchange separation: Isolation/Purification Techniques: CB, separation method; matrix assisted laser-desorption ionization mass **spectrometry**: analytical method, spectroscopic techniques: CB; model 473A pulse-liquid Edman degradation sequencer: Applied Biosystems, equipment; model 494A pulse-liquid Edman degradation sequencer: Applied Biosystems, equipment; reversed-phase **chromatography**: Isolation/Purification Techniques: CB, purification method; Edman sequencing: sequencing method, sequencing techniques; LaserTec RBT matrix assisted laser desorption ionization mass **spectrometer**: Perseptive/Vestec, equipment; Vydac reversed-phase column **chromatograph**: equipment
ORGN Super Taxa
Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
porcine (Suidae)
ORGN Organism Superterms
Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates

L57 ANSWER 2 OF 5 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:396353 BIOSIS

DN PREV199900396353
TI Strategy for identifying circulating fragments of insulin-like growth factor binding **proteins** in a hemofiltrate **peptide bank**.
AU Mark, Silke; **Forssmann, Wolf-Georg**; Staendker, Ludger (1)
CS (1) Lower Saxony Institute for Peptide Research (IPF), Feodor-Lynen Strasse 31, D-30625, Hannover Germany
SO Journal of Chromatography A, (Aug. 6, 1999) Vol. 852, No. 1, pp. 197-205. ISSN: 0021-9673.
DT Article
LA English
SL English
AB A differentiated strategy was established to isolate circulating forms of the six human insulin-like growth factor binding **proteins** (IGFBPs). As starting material we used our **peptide** bank, a comprehensive blood plasma peptidoma generated from human blood filtrate. The **peptides** were initially identified in the fractions of the hemofiltrate **peptide** bank by their immunoreactivity, their capacity to bind the insulin-like growth factors (IGFs), and their molecular masses determined by polyacrylamide gel electrophoresis and matrix-assisted laser desorption ionization-mass **spectrometry** (MALDI-MS). Fractions revealing both immunoreactivity and IGF-binding capacity were analyzed by direct sequencing of immunoreactive bands from a Coomassie-stained gel. Further purification of the IGFBP **peptides** was performed by consecutive **chromatographic** steps guided by sensitive MALDI-MS. Using this strategy, different fragments of IGFBP-3, -4, and -5 were identified and a fragment of IGFBP-4 was purified tohomogeneity.
CC Biochemical Studies - General *10060
Biochemical Methods - General *10050
Biophysics - General Biophysical Studies *10502
BC Hominidae 86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
insulin-like growth factor binding **protein**-3: analysis, circulating fragments, isolation; insulin-like growth factor binding **protein**-4: analysis, isolation, circulating fragments; insulin-like growth factor binding **protein**-5: analysis, isolation, circulating fragments; insulin-like growth factor binding **proteins**: analysis, circulating fragments, isolation
IT Methods & Equipment
immunoblotting: Detection/Labeling Techniques, analytical method; liquid **chromatography**: **chromatographic** techniques, isolation method; matrix assisted laser desorption ionization mass **spectrometry**: analytical method, spectroscopic techniques: CB; LaserTec RBT II mass spectroscope: PerSeptive Biosystems, equipment; SDS-PAGE [SDS-polyacrylamide gel electrophoresis]: polyacrylamide gel electrophoresis, purification method; Voyager-DE STR spectroscope: PerSeptive Biosystems, equipment
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L57 ANSWER 3 OF 5 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:256439 BIOSIS
DN PREV199900256439
TI Composition of the **peptide** fraction in human blood plasma: **Database** of circulating human **peptides**.
AU Richter, Rudolf (1); **Schulz-Knappe, Peter; Schrader, Michael**; Staendker, Ludger; Juergens, Michael; Tammen, Harald; **Forssmann, Wolf-Georg**
CS (1) Lower Saxony Institute for Peptide Research, Feodor-Lynen-Strasse 31,

D-30625, Hannover Germany
SO Journal of Chromatography B, (April 16, 1999) Vol. 726, No. 1-2, pp. 25-35.
ISSN: 0378-4347.
DT Article
LA English
SL English
AB A **database** was established from human hemofiltrate (HF) that consisted of a mass **database** and a sequence **database**, with the aim of analyzing the composition of the **peptide** fraction in human blood. To establish a mass **database**, all 480 fractions of a **peptide** bank generated from HF were analyzed by MALDI-TOF mass **spectrometry**. Using this method, over 20 000 molecular masses representing native, circulating **peptides** were detected. Estimation of repeatedly detected masses suggests that approximately 5000 different **peptides** were recorded. More than 95% of the detected masses are smaller than 15 000, indicating that HF predominantly contains **peptides**. The sequence **database** contains over 340 entries from 75 different **protein** and **peptide** precursors. 55% of the entries are fragments from plasma **proteins** (fibrinogen A 13%, albumin 10%, mu2-microglobulin 8.5%, cystatin C 7%, and fibrinogen B 6%). Seven percent of the entries represent **peptide** hormones, growth factors and cytokines. Thirty-three percent belong to **protein** families such as complement factors, enzymes, enzyme inhibitors and transport **proteins**. Five percent represent novel **peptides** of which some show homology to known **peptide** and **protein** families. The coexistence of processed **peptide** fragments, biologically active **peptides** and **peptide** precursors suggests that HF reflects the **peptide** composition of plasma. Interestingly, **protein** modules such as EGF domains (meprin Aalpha-fragments), somatomedin-B domains (vitronectin fragments), thyroglobulin domains (insulin like growth factor-binding **proteins**), and Kazal-type inhibitor domains were identified. Alignment of sequenced fragments to their precursor **proteins** and the analysis of their cleavage sites revealed that there are different processing pathways of plasma **proteins** in vivo.
CC Blood, Blood-Forming Organs and Body Fluids - General; Methods *15001
Biochemical Methods - General *10050
Biochemical Studies - General *10060
BC Hominidae 86215
IT Major Concepts
Blood and Lymphatics (Transport and Circulation); Methods and Techniques
IT Parts, Structures, & Systems of Organisms
blood plasma: blood and lymphatics
IT Chemicals & Biochemicals
albumin; beta-2-microglobulin; cystatin C; cytokines; cDNA [complementary DNA]; fibrinogen A; fibrinogen B; growth factors; human hemofiltrate: Nephrologisches Zentrum Niedersachsen; **peptide** hormones; **peptides**; somatomedin-B; thyroglobulin
IT Methods & Equipment
alginic acid exchanger: Merck, laboratory equipment; amino acid sequencing: Recombinant DNA Technology, gene sequencing method, sequencing techniques; cation exchange **chromatography**: column **chromatography**, isolation method; **peptide** extraction: Isolation/Purification Techniques: CB, extraction method; reversed-phase **chromatography**: **chromatographic** techniques, isolation method; strong cation exchanger: Merck, laboratory equipment; Autopilot **chromatography** system: PerSeptive Biosystems, laboratory equipment; API III-plus triple quadrupol-MS system: PE Sciex Instruments, laboratory equipment; LaserTec RBT II MALDI-TOF-MS system: Perseptive/Vastec, laboratory equipment; Model 473 A gas-phase sequencer: Applied Biosystems, laboratory equipment; Model 494 A gas-phase sequencer: Applied Biosystems, laboratory equipment; MALDI-TOF mass **spectrometry**

[matrix-assisted laser/desorption ionization-time-of-flight mass **spectrometry**]: analytical method, mass **spectrometry**: CB

IT Miscellaneous Descriptors
amino acid sequence

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae)

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

RN 91448-99-6 (CYSTATIN C)
63774-77-6 (SOMATOMEDIN-B)
9005-32-7 (ALGINIC ACID)

L57 ANSWER 4 OF 5 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1997:433466 BIOSIS

DN PREV199799732669

TI **Peptide bank** generated by large-scale preparation of circulating human **peptides**.

AU **Schulz-Knappe, Peter (1); Schrader, Michael;** Staendker, Ludger; Richter, Rudolf; Hess, Ruediger; Juergens, Michael; **Forssmann, Wolf-Georg**

CS (1) Niedersaechsisches Inst. Peptid-Forschung GmbH, Feodor-Lynen-Strasse 31, 30625 Hannover Germany

SO Journal of Chromatography A, (1997) Vol. 776, No. 1, pp. 125-132. ISSN: 0021-9673.

DT Article

LA English

AB Human hemofiltrate (HF) is a source for the purification of circulating regulatory **peptides**. HF is obtained in large quantities during treatment of patients suffering from chronic renal failure. We have developed a large-scale method for separating **peptides** from amounts up to 10 000 1 HF into 300 fractions in a standardized two-step procedure, employing cation-exchange separation, followed by reversed-phase **chromatography**. These fractions represent a **peptide** bank containing bioactive, desalted and lyophilized **peptides** of blood. Screening for and isolation of regulatory human **peptides** is simplified by using this **peptide** bank.

CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504

BC Hominidae *86215

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Miscellaneous Descriptors
BIOCHEMISTRY AND BIOPHYSICS; HEMOFILTRATE; METHODOLOGY; **PEPTIDE BANK**; **PEPTIDES**; PURIFICATION METHOD; REVERSED-PHASE **CHROMATOGRAPHY**

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae)

ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L57 ANSWER 5 OF 5 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1997:433465 BIOSIS

DN PREV199799732668

TI **Mapping** of **peptides** and **protein** fragments in human urine using liquid **chromatography**-mass **spectrometry**.

AU Heine, Gabriele; Raida, Manfred (1); **Forssmann, Wolf-George**

CS (1) Lower Saxony Inst. Peptide Res., Feodor-Lynen-Strasse 31, D-30625 Hannover Germany

SO Journal of Chromatography A, (1997) Vol. 776, No. 1, pp. 117-124.

ISSN: 0021-9673.
DT Article
LA English
AB A method for the mapping of **peptide** mixtures, heterogeneous with respect to the concentration and the size of individual **peptides**, was established with the aim of obtaining a comprehensive analysis of human urine **peptides**. **Peptide** extraction and fractionation were optimized to achieve a two-step analysis, using reversed-phase and ion-exchange **chromatography**. Highly sensitive detection of **peptides** was performed by coupling microbore HPLC with electrospray mass **spectrometry** (ESI-MS). **Peptides** such as urodilatin, angiotensin and fragments of psoriasin, granulin and uromodulin were isolated and sequenced. The procedure presented here is a tool for the analysis of complex **peptide** mixtures from human urine.
CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Urinary System and External Secretions - Physiology and Biochemistry *15504
BC Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Urinary System (Chemical Coordination and Homeostasis)
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND BIOPHYSICS; EXCRETORY SYSTEM; HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**-ELECTROSPRAY MASS **SPECTROMETRY**; METHODOLOGY; **PEPTIDES**; **PROTEIN** FRAGMENTS; URINARY SYSTEM; URINE
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

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                  E FORSSMAN/AU
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                  E FORSMAN/AU
                  E OPITZ/AU
L3             60 S E13,E15
                  E SCHRADER M/AU
L4             19 S E3-E8
                  E SCHULZ KNAP/AU
L5             18 S E4,E5
L6            116 S L2-L5
L7           4056 S G01N033-68/IC,ICM,ICS,ICA,ICI
L8             10 S L6 AND L7
L9              9 S L8 AND S03-E14H?/MC
L10             1 S L8 NOT L9
L11             9 S L1,L9
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L13           663 S (M423 (S) M760 (S) N102 (S) Q233 (S) (V600 OR V644) (S) V754)
L14             1 S L6 AND L12,L13
L15             9 S L11,L14
L16          1093 S L12,L13
L17           130 S L7 AND L16
L18         26866 S (B04-F01 OR B04-B02 OR B04-B02B OR B04-B04 OR B04-B04A OR B04
L19          7429 S (C04-F01 OR C04-B02 OR C04-B02B OR C04-B04 OR C04-B04A OR C04
L20           696 S L7 AND L18,L19
L21           547 S L20 AND S03-E14H?/MC
L22           592 S L20 AND (B12-K04 OR B12-K04A OR C12-K04 OR C12-K04A OR D05-H0
L23           666 S L21,L22
L24           758 S L17,L23
L25           643 S L24 AND S03/DC
L26             0 S L25 AND (?MALDI? OR MATRIX(L)ASSIS?(L)LASER(L)DESORPT?(L)IONI
L27             2 S L7 AND (?MALDI? OR MATRIX(L)ASSIS?(L)LASER(L)DESORPT?(L)IONI?
L28             4 S L7 AND (?ELECTROSPRAY? OR ?ELECTRO SPRAY?)
L29             0 S L7 AND (ESIMS OR ESI MS OR ESI MASS SPECTROM?)
L30             0 S L7 AND (?MICROBORE? OR ?MICRO BORE?)
L31            24 S L7 AND LOW MOLECULAR WEIGHT
L32             3 S L31 AND L16
L33             6 S L31 AND L20
L34            12 S L32,L33,L27,L28
L35            20 S L15,L34
L36            17 S L31 NOT L35
L37            37 S L35,L36
L38            36 S L37 AND G01N033-68/IC,ICM
L39            10 S L37 AND G01N033-68/ICM
L40            27 S L37 NOT L39
L41             6 S L39 NOT (VENOM OR ARTHRITIC OR CALMODULIN OR ISOTHIOCYANATE)/
L42             1 S L40 AND (DETECTION AND ANALYTE#)/TI
L43             1 S L40 AND (STRUCTURAL ANALYSIS)/TI
L44             1 S L40 AND (ISOLAT? AND CHROMATOG?)/TI
L45             1 S L40 AND (IMMOBIL? AND VAPOUR)/TI
L46            16 S L15,L41-L45
L47            63 S L25 AND MOLECULAR WEIGHT
L48            58 S L47 NOT L31
L49             1 S L48 AND IMMUNOGLOBULIN/TI
L50           633 S L24 AND S03-E14?/MC
L51           758 S L24,L50
L52             1 S L51 AND ?CHROMATOG? AND ?SPECTROMET?
L53            10 S L7 AND ?CHROMATOG? AND ?SPECTROMET?
L54            18 S L46,L49,L52
L55             7 S L53 NOT L54
L56             2 S L51 AND REVERSE (L) (?CHROMATOG? OR ?SPECTROM?)

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L54 ANSWER 1 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1999-591377 [50] WPIDS
CR 1998-570290 [49]; 1999-591376 [49]
DNN N1999-436154 DNC C1999-172815
TI Screening for compounds with affinity for target receptors, using target receptors on a column, frontal **chromatography** and mass **spectrometry**.
DC B04 D16 J04 S03 V05
IN HINDSGAUL, O; SCHRIEMER, D C
PA (SYNS-N) SYNSORB BIOTECH INC
CYC 86
PI WO 9950669 A1 19991007 (199950)* EN 89p G01N033-68 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW
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ADT WO 9950669 A1 WO 1999-CA266 19990326
PRAI US 1998-70131 19980429; US 1998-79622 19980327
IC ICM **G01N033-68**
ICS G01M003-20; G01N033-538; G01N033-543; H01J049-26
AB WO 9950669 A UPAB: 19991201
NOVELTY - Method for screening for compounds with affinity for target receptors uses frontal **chromatography** and mass **spectrometry**.

DETAILED DESCRIPTION - (A) Method for screening a compound library to determine the relative or absolute affinity of putative ligands to a target receptor (TR) or TRs comprises:

(a) providing a compound library comprising putative ligands;

(b) applying the compound library to a column comprising a TR or TRs, each TR optionally bound to a solid phase support, under frontal **chromatography** conditions to provide an effluent;

(c) continuously or intermittently applying the effluent to a mass **spectrometer** to provide mass spectra of the constituent putative ligands present in the effluent; and

(d) evaluating the mass spectra to determine a break through time for the putative ligands.

INDEPENDENT CLAIMS are also included for:

(1) a method for screening compound libraries to determine the relative affinity of putative ligands in each library to a TR or TRs, comprising: (a) step (a) and (b) as in (A); (b) intermittently applying the effluent from each column to a mass **spectrometer** to provide spectra of the constituent putative ligands present in the effluent; and (d) evaluating the mass spectra to determine a break through time for the putative ligands in each compound library;

(2) a method for screening a compound library to determine the relative affinity of putative ligands to a TR or TRs relative to an indicator compound or compounds, comprising: (a) providing a compound library comprising putative ligands; (b) providing at least one void marker compound; (c) providing an indicator compound or compounds for each TR, each indicator compound having a pre-determined affinity for the TR and a pre-determined break through time on the column in the absence of the compound library relative to a void marker compound; (d) applying the compound library to a column comprising a TR or TRs, each TR optionally bound to a solid phase support, under frontal **chromatography** conditions to equilibrate or partially equilibrate the column with the compound library; (e) applying (i) a mixture comprising the compound library, the void marker compound and the indicator compound or compounds, or (ii) the void marker compound and the indicator compound or compounds, to the column under frontal **chromatography** to provide an effluent; (f) analyzing the effluent to determine a break through time for the indicator compound or compounds;

(3) a method for screening a compound library to determine the relative affinity of putative ligands to a TR relative to an indicator compound having a pre-determined affinity for the TR, comprising: (a) steps (a)-(d) as in (2); (b) applying a mixture comprising the compound library and the indicator compound to the column under frontal **chromatography** conditions to provide an effluent; (c) analyzing the effluent to determine a break through time and/or signal intensity for the indicator compound;

(4) a method for screening a compound library to identify inhibitors of a TR, comprising: (a) providing a compound library comprising putative ligands; (b) applying the compound library to a column comprising a TR optionally bound to a solid phase support under frontal **chromatography** conditions to equilibrate or partially equilibrate the column with the compound library; (c) providing a first indicator compound which is capable of being chemically modified by the TR to form a second indicator compound; (d) applying (i) a mixture comprising the compound library and the first indicator compound, or (ii) the first indicator compound, to the column under frontal **chromatography** conditions to provide an effluent; (e) analyzing the effluent to determine the presence and/or concentration of the second indicator compound;

(5) a method for screening a TR or TRs to determine the relative affinity of the receptor or receptors to an immobilized ligand or ligands relative to an indicator compound or compounds, comprising: (a) providing a TR or TRs; (b) providing a column comprising a ligand or ligands, each bound to a solid phase support; (c) providing at least one void marker compound; (d) providing an indicator compound or compounds for each ligand, each indicator compound having a pre-determined affinity for the ligand and having a pre-determined break through time on the column relative to a void marker compound; (e) applying the TR or TRs to the column under frontal **chromatography** conditions to equilibrate or partially equilibrate the column with the TRs or receptors; (f) applying (i) a mixture comprising the TR or TRs, the void marker compound and the indicator compound or compounds, or (ii) the void marker compound and the indicator compound or compounds, to the column under frontal **chromatography** conditions to provide an effluent; (g) analyzing the effluent to determine a break through time for the indicator compound or compounds.

USE - The methods can be used for identifying compounds which bind to TRs and determine the relative affinity for the TRs.

ADVANTAGE - Using the methods, an accurate ranking of the relative affinity of each member of the compound library for the target receptor can be ascertained. Several frontal **chromatography**-mass **spectrometry** (FC-MS) assays can be conducted simultaneously using a single mass **spectrometer** to intermittently monitor each column.

Dwg.0/16

FS CPI EPI

FA AB; DCN

MC CPI: B03-A; B04-B01B; B04-B03; B04-C01; B04-E01; **B04-F01**; B04-F08; B04-F10; B04-F11; B04-G01; B04-H01; B04-J01; B04-J02; B04-K01; B04-L01; B04-N04; B04-N06; B06-F03; B11-C07B3; B11-C08A; B11-C08D2; B11-C08E3; **B12-K04**; D05-A01C1; D05-A02; D05-A03A; **D05-H09**; D05-H10; D05-H12; J04-B01A; J04-B01C

EPI: S03-E09C7B; S03-E10A; **S03-E14H**; **S03-E14H4**; V05-J01A1; V05-J01K

L54 ANSWER 2 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

AN 1999-591376 [50] WPIDS

DNN N1999-436153 DNC C1999-172814

TI **Electrospray** device for mass spectrometer,.

DC J04 S03 V05

IN HINDSGAUL, O; SCHRIEMER, D C

PA (SYNS-N) SYNSORB BIOTECH INC

CYC 86

PI WO 9950667 A1 19991007 (199950)* EN 28p G01N033-68 <--

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL

OA PT SD SE SL SZ UG ZW
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW

ADT WO 9950667 A1 WO 1999-CA264 19990326
PRAI US 1998-69656 19980429; US 1998-79622 19980327
IC ICM **G01N033-68**
ICS B01D059-44; G01M003-20; G01N033-538; G01N033-543; H01J049-02; H01J049-10; H01J049-26
AB WO 9950667 A UPAB: 19991201
NOVELTY - The **electrospray** device has a number of **electrospray** needles (10) mounted on a support in a circular arrangement. The needles can be connected to a number of sample streams for delivery of droplets of the sample streams to a mass spectrometer orifice (22). A rotatable member directs droplets from one sample stream at a tine to the orifice. A charger applies a charge to the droplets of the sample stream and causes ions to be focused into a beam passing through the orifice.

DETAILED DESCRIPTION - Preferred Features: Preferably the needles are mounted on a rotatable disk (12) with their axes parallel and in a radial arrangement. An INDEPENDENT CLAIM is included for a method of delivering a number of sample streams to a mass spectrometer for sequential analysis.

USE - For delivering multiple liquid sample streams to a mass spectrometer, such as for analysis of compound libraries.

ADVANTAGE - This **electrospray** device enables streams from multiple chromatography columns or other sample sources to be easily connected for intermittent analysis, and can move from one sample to another automatically to analyze a number of samples in as short a time as possible.

DESCRIPTION OF DRAWING(S) - The drawing shows a side view of a multiple needle **electrospray** apparatus for delivery of sample streams to a mass spectrometer.

Electrospray needles 10
Rotatable plate 12
Mass spectrometer entry orifice 22

Dwg.1/8
FS CPI EPI
FA AB; GI
MC CPI: J04-B01A
EPI: S03-E09C7B; S03-E10A; S03-E13B1; S03-E14H; V05-J01A1; V05-J01K

L54 ANSWER 3 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1999-527189 [44] WPIDS
DNN N1999-390515 DNC C1999-154792
TI New inhibitors of serine protease useful for treating inflammation.
DC B04 D16 S03
IN **FORSSMANN, W**; KREUTZMANN, P; MAEGERT, H; STAENDKER, L
PA (FORS-I) FORSSMANN W
CYC 21
PI WO 9933974 A1 19990708 (199944)* DE 40p C12N015-12
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP US
DE 19800363 A1 19990715 (199944) C07K014-81
ADT WO 9933974 A1 WO 1998-EP8424 19981223; DE 19800363 A1 DE 1998-19800363 19980108
PRAI DE 1998-19800363 19980108; DE 1997-19757572 19971223
IC ICM C07K014-81; C12N015-12
ICS A61K031-70; A61K038-55; A61K038-57; A61K039-395; A61K048-00; C07H021-04; C07K016-38; C12N015-11; C12N015-15; **G01N033-68**
AB WO 9933974 A UPAB: 19991026
NOVELTY - Serine protease inhibitor (I) includes a domain with four Cys residues with the numbers of amino acids (aa) between the first (Cys1) and second (Cys2), the second and third (Cys3), and the third and fourth (Cys4) being 13, 18 and 2, respectively.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the

following:
(1) nucleic acid (II) that encodes (I);
(2) pharmaceutical composition containing (I) and/or (II), optionally also a carrier;
(3) antibody (Ab), or its fragments, directed against epitopes on (I);
(4) antisense poly- or oligo-nucleotides (III) that hybridize under stringent conditions to (I)-encoding cDNA or RNA, and optionally inhibiting expression of the corresponding genes;
(5) diagnostic and pharmaceutical compositions containing Ab, or its fragments, and/or (III); and
(6) DNA encoding (I) and/or RNA involved in transcription or translation of (I).
ACTIVITY - Antiinflammatory.
MECHANISM OF ACTION - Inhibition of serine proteases such as trypsin. The 65 aa inhibitor designated HF7665, at 75 mu g/ml, caused about 30% inhibition of trypsin when tested in pH 7.5 buffer with N alpha -benozyl-L-Arg-p-nitroanilide as substrate.
USE - (I) are used to treat acute or chronic cervical inflammation, inflammation of the Bartholin glands and other vaginal regions, tonsillitis, pharyngitis, laryngitis, inflammation involving excessive secretion of mucus (including acute, emergency episodes), post-operative bleeding as a result of excessive fibrinolysis, and for preventing pulmonary emphysema caused by lack of alpha 1-proteinase inhibitor. (I) may also be used to raise antibodies (Ab) and Ab or antisense nucleic acid directed against sequences that encode (II) can be used as diagnostic agents, also therapeutically in cases of overexpression of (I).
Dwg.0/3
FS CPI EPI
FA AB; DCN
MC CPI: B04-C01G; B04-E02F; B04-E03F; B04-G01; B12-K04; B14-C03; B14-D03; B14-D07C; B14-K01; B14-N05; B14-N14; D05-H09; D05-H11; D05-H12A; D05-H12D2
EPI: **S03-E14H**

L54 ANSWER 4 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1999-312406 [26] WPIDS
DNN N1999-233324 DNC C1999-092182
TI Mass spectrometry detection of polypeptides useful for determining genetic predispositon to Huntington's disease and prostate cancer.
DC B04 D16 J04 S03
IN HIGGINS, G S; KOESTER, H; LITTLE, D; LOUGH, D
PA (SEQU-N) SEQUENOM INC
CYC 81
PI WO 9912040 A2 19990311 (199926)* EN 69p G01N033-68 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW
AU 9891298 A 19990322 (199931) G01N033-68 <--
ADT WO 9912040 A2 WO 1998-US18311 19980902; AU 9891298 A AU 1998-91298 19980902
FDT AU 9891298 A Based on WO 9912040
PRAI US 1997-922201 19970902
IC ICM **G01N033-68**
AB WO 9912040 A UPAB: 19990707
NOVELTY - Process (M1) for determining the identity of a target polypeptide (P1), using mass spectrometry (MS) to determine the molecular mass (MW), and comparing this with molecular mass of a known polypeptide, is new.
DETAILED DESCRIPTION - M1 comprises:
(a) obtaining the polypeptide by in vitro translation, or transcription then translation, of a nucleic acid encoding the polypeptide;

(b) determining the MW of at least one of the obtained fragments by MS; and

(c) comparing the fragment(s) MW with the MW of fragments of a corresponding known polypeptide.

INDEPENDENT CLAIMS are also included for the following:

(1) a kit for determining the identity of (P1) by MS;

(2) a method for screening for or identifying a subject having or predisposed to a disease or condition, comprising:

(a) obtaining a target polypeptide which is a marker for the disease from a biological sample of subject, either directly or via nucleic acid;

(b) determining the MW of the target polypeptide by MS;

(c) comparing the MW of the target with a corresponding known polypeptide;

(3) a process for determining the amino acid sequence of a polypeptide using MS, comprising:

(a) contacting the polypeptide with an agent that cleaves an amino acid from the polypeptide terminus to produce a cleaved amino acid and a deletion fragment;

(b) subjecting the cleaved amino acid or the deletion fragment to MS; and

(c) repeating steps (a) and (b) as necessary to determine the polypeptide sequence; and

(4) a process for determining a nucleotide sequence of an unknown polynucleotide using MS, comprising:

(a) determining the amino acid sequence of a polypeptide encoded by the unknown polynucleotide using the method of (3);

(b) comparing the amino acid sequence to an amino acid sequence encoded by a corresponding known polynucleotide.

USE - The methods are used to detect the presence or disposition for genetic diseases or conditions particularly those caused by an abnormal number of trinucleotide repeats in a gene, such as Huntington's disease, prostate cancer, Fragile X syndrome type A, myotonic dystrophy type I, Kennedy disease, Machado-Joseph disease, and dentatorubral or pallidolyusian atrophy, spino bulbar muscular atrophy or ageing, and also for genotyping, in forensic analysis and parental testing, where the nucleotide repeats, preferably di-, tri-, tetra-, or penta-nucleotide repeats, are quantified (claimed).

ADVANTAGE - Unlike prior art identification by nucleic acid probe, the invention does not require labeling of the nucleic acid, and unlike gel electrophoresis, where size of the polynucleotide cannot be directly related to mobility in the gel matrix, the invention allows reliable measurement of the encoded product which can then be related back to the polynucleotide. Mass spectrometry of the encoded polypeptide is advantageous over mass spectrometry of the polynucleotide, as nucleic acids are difficult to volatilize.

FS CPI EPI
FA AB; DCN
MC CPI: B04-C01; B11-C08A; B12-K04; D05-H09; D05-H10; D05-H11; D05-H12D1; D05-H18B; J04-B01A
EPI: S03-E10A; S03-E14H; S03-E14H5

L54 ANSWER 5 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1999-278856 [24] WPIDS
DNN N1999-208995 DNC C1999-082121
TI Gene for murine odorant binding protein.
DC B04 C06 D16 P14 S03
IN **FORSSMANN, W**; MAEGERT, H
PA (FORS-I) FORSSMANN W
CYC 1
PI DE 19756678 C1 19990520 (199924)* 17p C12N015-12
ADT DE 19756678 C1 DE 1997-19756678 19971219
PRAI DE 1997-19756678 19971219
IC ICM C12N015-12
ICS A01K067-027; C07H021-04; C12Q001-68; **G01N033-68**
AB DE 19756678 C UPAB: 19990624
NOVELTY - Gene (I), has a 7367 bp sequence reproduced, that encodes the

mouse odorant binding protein (II), or its allelic variants.
DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a transgenic rodent defective in (I).
ACTIVITY - None given.
MECHANISM OF ACTION - None given.
USE - (I) is used to design nucleic acids (particularly intron/exon junction segments) for 'switching off' the gene in rodents. Transgenic animals with a defect in (I) are used (i) to investigate fertility disorders and (ii) to identify pheromones or their transport proteins. Administration of (II), or its expression in vivo from cDNA corresponding to (I), can be used to study the effect of (II) on fertility.
FS CPI EPI GMPI
FA AB; DCN
MC CPI: B04-E01; C04-E01; D05-H12D; D05-H13
EPI: **S03-E14H**

L54 ANSWER 6 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1998-521398 [44] WPIDS
DNN N1998-407161 DNC C1998-156695
TI **Detection** of **low molecular weight analytes** - uses recombinant antibody fragments in homogeneous competition immunoassays.
DC A86 B04 C07 D16 E19 H04 J04 S03
IN GRANT, S; HARRIS, W; PORTER, A
PA (GRAN-I) GRANT S; (HARR-I) HARRIS W; (PORT-I) PORTER A
CYC 19
PI WO 9841871 A1 19980924 (199844)* EN 22p G01N033-563
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: JP US
ADT WO 9841871 A1 WO 1998-GB733 19980311
PRAI GB 1997-5376 19970314
IC ICM G01N033-563
ICS **G01N033-68**
AB WO 9841871 A UPAB: 19981210
Detection and measurement of **low molecular weight** (mol. wt.) analytes is carried out by incorporating recombinant antibody fragemnts (rAbFs) in homogenous competition immunoassays. Also claimed is a kit for carrying out the above mentioned method, where the kit is disposed in or on a contact surface and means for performing competitive or non-competitive ELISA assays or biosensor measurements.
The process is used for small mol. wt. analytes which can be trapped between capture and detector antibodies, e.g. pesticides, herbicides, insecticide drugs, oestrogenic mimetics, petroleum products, alkylphenolics, phthalates and organochlorines (all claimed).
ADVANTAGE - The immnoassay, using recombinant antibody fragments, provides improved sensitivity and specificity.
Dwg.0/7
FS CPI EPI
FA AB; DCN
MC CPI: A12-L04B; A12-V03C2; B04-G01; B07-D13; B10-C02; B10-C04C; B10-E02; B10-G02; B10-H02E; B10-H02F; B11-C07; B12-K04; D05-H09; D05-H11; H04-E; J04-B01
EPI: S03-E14H; S03-E14H4

L54 ANSWER 7 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1998-467556 [40] WPIDS
DNN N1998-364295 DNC C1998-141827
TI New human neutrophil-lymphocyte peptide and its fragments - used for treatment and diagnosis of inflammatory diseases, tumours and disorders of haematopoietic maturation.
DC B04 D16 S03
IN **FORSSMANN, W**; KLEEMEIER, B; NEHLS, M; **SCHULZ-KNAPPE, P**
PA (FORS-I) FORSSMANN W
CYC 19
PI WO 9837191 A1 19980827 (199840)* DE 41p C12N015-12

RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: JP US
DE 19730786 A1 19990121 (199909) C07K016-00
DE 19730786 C2 19991111 (199952) C07K014-435
ADT WO 9837191 A1 WO 1998-EP950 19980219; DE 19730786 A1 DE 1997-19730786 19970718; DE 19730786 C2 DE 1997-19730786 19970718
PRAI DE 1997-19730786 19970718; DE 1997-19706937 19970220; DE 1997-19712487 19970325
IC ICM C07K014-435; C07K016-00; C12N015-12
ICS A61K038-12; A61K038-17; A61K048-00; C07H021-00; C07K001-04; C07K001-18; C07K001-36; C07K007-64; C07K014-47; C07K016-18; C12N001-00; C12N005-10; C12N015-11; C12N015-63; C12N015-85; C12N015-86; C12Q001-68; **G01N033-68**
AB WO 9837191 A UPAB: 19981111
Peptides of formula (I) are new: Ra-C-Xn-C-Rd (I) Ra = amino or its derivative, or an oligo- or poly-peptide made from natural amino acids (aa), derivatives modified in the side chain and/or their stereoisomers; n = 3-7; X = natural aa as above; Rd = carboxy, its derivative or oligo- or poly-peptide as above. Also new are (1) nucleic acid (II) encoding (I), or its fragments, derivatives and analogues; (2) vectors containing (II); (3) host cells containing this vector; (4) DNA that hybridises with (II) and encodes a polypeptide with human neutrophil-lymphocyte peptide (hNLP) activity; (5) antibody (Ab), antagonist or inhibitor directed against (I); (6) antisense oligonucleotide (AON) that inhibits hNLP expression; (7) vector for producing knock-out mice as a chronic model of maturation disorders of the haematopoietic system.
USE - (I) and (II) are used to treat inflammatory disease, tumours and disorders of haematopoietic proliferation and maturation, while Ab, antagonists, inhibitors and AON are used to treat infections, inflammation, and proliferative or neoplastic diseases of e.g. the respiratory or gastrointestinal (GI) tracts, urogenital systems and particularly the haematopoietic system.(I) and Ab are also used diagnostically to detect diseases of bone marrow, lymphatic organs, the GI tract and immune systems, also inflammatory and neoplastic disease. (I) is an anti-proliferative agent similar to known interleukins.
Dwg.0/0
FS CPI EPI
FA AB; DCN
MC CPI: B04-C01F; B04-E05; B04-E08; B04-L05; B11-C07A; B12-K04A; B14-C03; B14-E10; B14-H01; B14-H01B; B14-N07; D05-H09; D05-H11; D05-H12A; D05-H12D2; D05-H12E; D05-H14; D05-H16A; D05-H17A
EPI: **S03-E14H**

L54 ANSWER 8 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1998-159670 [14] WPIDS
CR 1998-131295 [13]
DNN N1998-126827 DNC C1998-051622
TI Determining status of organism by measuring **low molecular weight** peptide(s) - indicative of status, particularly for diagnosis, toxicological analysis, identifying gene products etc..
DC B04 C07 D16 S03
IN **FORSSMANN, W; OPITZ, H; SCHRADER, M; SCHULZ-KNAPPE, P**
PA (FORS-I) FORSSMANN W; (BIOV-N) BIOVISION GMBH & CO KG
CYC 71
PI WO 9807036 A1 19980219 (199814)* DE 23p G01N033-68 <--
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
W: AL AU BA BB BG BR BY CA CN CU CZ DE EE GE HU IL IS JP KP KR LC LK LR LT LV MG MK MN MX NO NZ PL RO SG SI SK SL TR TT UA US UZ VN YU
AU 9742988 A 19980306 (199830) G01N033-68 <--
EP 922226 A1 19990616 (199928) DE G01N033-68 <--
R: AT BE CH DE DK ES FR GB IE IT LI LT LU LV NL PT RO SE SI
ADT WO 9807036 A1 WO 1997-EP4396 19970813; AU 9742988 A AU 1997-42988 19970813; EP 922226 A1 EP 1997-918977 19970813, WO 1997-EP4396 19970813

FDT AU 9742988 A Based on WO 9807036; EP 922226 A1 Based on WO 9807036
PRAI DE 1997-19725362 19970616; DE 1996-19632521 19960813
IC ICM **G01N033-68**
AB WO 9807036 A UPAB: 19980406
Determining the status of an organism comprises direct measurement and characterisation of indicative **low molecular weight** (mol. wt.) peptides (I) in a sample and comparing the results with a reference. The sample from the organism contains (I) and high mol. wt. peptides.

USE - The method is used for hypothesis-free investigations of the status of the whole organism; for detecting any anomalies from the reference condition and, for transfected organisms, identification of potentially toxic peptides associated with altered metabolism caused by the transfection.

Typical applications are in clinical studies (identifying disease states); toxicological analysis; determination of breakdown products and identification of gene products, in human or veterinary medicine.

ADVANTAGE - The method is universally applicable (including use on lower organisms) and is easily set up using standard procedures. Single, or many (I), can be detected directly; contrast indirect methods such as immunoassays.

Dwg.0/0
FS CPI EPI
FA AB
MC CPI: **B04-F01**; **C04-F01**; B04-N04; C04-N04; B12-K04A; C12-K04A; D05-H09
EPI: **S03-E14H**

L54 ANSWER 9 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1998-131295 [13] WPIDS
CR 1998-159670 [14]
DNN N1998-103636 DNC C1998-043465
TI **Isolating** peptide(s) from body fluids, tissues and cell supernatant - by ultrafiltration then **chromatography**, particularly for identifying compounds characteristic of disease.
DC B04 D16 J04 S03
IN **FORSSMANN, W; OPITZ, H; SCHULZ-KNAPPE, P**
PA (FORS-I) FORSSMANN W
CYC 1
PI DE 19632521 A1 19980219 (199813)* 5p C07K014-435
ADT DE 19632521 A1 DE 1996-19632521 19960813
PRAI DE 1996-19632521 19960813
IC ICM C07K014-435
ICS C07K001-18; C07K001-34; G01N033-53; **G01N033-68**
AB DE 19632521 A UPAB: 19980406
Production of peptide fractions (A) from body fluids, tissue or cell supernatant comprises ultrafiltration (UF); ion-exchange extraction (IEE); pH elution; reverse-phase separation and freeze-drying.

USE - The method is used:
(i) to map peptides from fluids or tissues;
(ii) to prepare samples for chromatography/mass spectrometric (MS) analysis for comparative analysis of peptide spectra;
(iii) to identify peptide markers of disease;
(iv) to purify peptides defined by mapping;
(v) for diagnosis, from changes in the peptide spectrum, of tumours, systemic, cardiac-circulatory or immune system diseases, or osteoporosis, or
(vi) to develop detection methods for peptides (such as enzyme-linked immunosorbent assay, radioimmunoassay and liquid chromatography/MS (LC-MS)).

Dwg.0/0
FS CPI EPI
FA AB
MC CPI: B04-C01; B11-C07; B11-C08; B12-K04A; D05-H13; J04-B
EPI: **S03-E14H**; **S03-E14H4**

L54 ANSWER 10 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1998-053368 [06] WPIDS
DNN N1998-042165 DNC C1998-018496
TI Diagnostic detection of pathogenic point mutation(s) - in e.g. heart disease, by protein analysis of expressions of prepared biopsies.
DC B04 D16 S03
IN BRENNER, B; **FORSSMANN, W**; NIER, V; RAIDA, M
PA (FORS-I) FORSSMANN W; (HAEM-N) HAEMOPEP PHARMA GMBH
CYC 20
PI DE 19624802 A1 19980102 (199806)* 4p C12Q001-24
WO 9749993 A1 19971231 (199807) DE 29p G01N033-68 <--
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: JP US
EP 914615 A1 19990512 (199923) DE G01N033-68 <--
R: AT CH DE FR GB IT LI
ADT DE 19624802 A1 DE 1996-19624802 19960621; WO 9749993 A1 WO 1997-EP3241 19970620; EP 914615 A1 EP 1997-929238 19970620, WO 1997-EP3241 19970620
FDT EP 914615 A1 Based on WO 9749993
PRAI DE 1996-19624802 19960621
IC ICM C12Q001-24; **G01N033-68**
ICS G01N021-00; G01N030-72
AB DE 19624802 A UPAB: 19980209
The following are claimed:
(1) ''use of the described method according to the invention for medical-diagnostic detection of the expression and incorporation of wild type besides mutants at the protein level in preparations that have been obtained from biopsies of human or animal tissue'';
(2) ''use of the described method for medical-diagnostic quantification of the expression and incorporation in physiologically functional structures of wild type and mutants at the protein level'';
(3) ''use of the described method for the medical-diagnostic analysis of the expression and incorporation and the ratio of wild type to mutants in various tissue and organ regions'';
(4) ''use of the method for medical-diagnostic analysis of biopsy samples that are present in only very small amounts'',
(5) ''use of the described method for medical-diagnostic detection of previously unknown pathogenic and non-pathogenic mutations directly at the protein level''.
N.B. No specific method has been provided.
USE - The methods are used to detect point mutations in proteins of human and animal organisms by analysing the heavy chains of the beta -isoform of muscle myosin using chemical and physical methods.
ADVANTAGE - The methods are far shorter in duration (1 week) than DNA analysis (many weeks).
Dwg.0/0
FS CPI EPI
FA AB
MC CPI: B04-E03; B04-N04; B11-C; B12-K04A; D05-H09
EPI: S03-E10A; **S03-E14H**

L54 ANSWER 11 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1997-514492 [48] WPIDS
DNN N1997-427947 DNC C1997-164493
TI Protein HF-COLL-18/514cf - useful for treating, e.g. diseases of supporting or connective tissue, respiratory or urogenital tract or of the cardiovascular or nervous system.
DC B04 D16 S03
IN **FORSSMANN, W**; RAIDA, M; **SCHRADER, M**; **SCHULZ-KNAPPE, P**; STANDKER, L; **FORSSMANN, W G**; STAENDKER, L
PA (FORS-I) FORSSMANN W; (HAEM-N) HAEMOPEP PHARMA GMBH
CYC 69
PI DE 19615710 A1 19971023 (199748)* 6p C07K014-78
WO 9740073 A2 19971030 (199749) DE 18p C07K014-78
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG

W: AL AU BA BB BG BR CA CN CU CZ EE GE GH HU IL IS JP KG KP KR LC LK LR LT LV MG MK MN MX NO NZ PL RO SG SI SK TR TT UA US UZ VN YU

AU 9727665 A 19971112 (199811) C07K014-78
WO 9740073 A3 19971224 (199817) C07K014-78
EP 896584 A2 19990217 (199912) DE C07K014-78
R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

ADT DE 19615710 A1 DE 1996-19615710 19960422; WO 9740073 A2 WO 1997-EP2012 19970422; AU 9727665 A AU 1997-27665 19970422; WO 9740073 A3 WO 1997-EP2012 19970422; EP 896584 A2 EP 1997-921682 19970422, WO 1997-EP2012 19970422

FDT AU 9727665 A Based on WO 9740073; EP 896584 A2 Based on WO 9740073

PRAI DE 1996-19615710 19960422

REP No-SR.Pub; 3.Jnl.Ref; DE 3633797; WO 9316716; WO 9715666

IC ICM C07K014-78
ICS A61K038-39; A61K039-395; C07K001-16; C07K016-18; G01N033-53; **G01N033-68**

AB DE 19615710 A UPAB: 19971209
Protein HF-COLL-18/514cf with the N-terminal amino acid sequence (A) is new: Val-Ala-Arg-Asn-Ser-Pro-Leu-Ser -Gly-Gly-Met-Arg-Gly-Ile-Arg-Gly-Ala-Asp-Phe-Gln-Cys-Phe-Gln-Gln-Ala-Arg-Ala-Val-Gly-Leu (A). Natural and pharmacologically acceptable derivatives of (A) are also included, especially amidated, acetylated, phosphorylated and glycosylated derivatives, and natural and synthetic fragments with biological activity derived from the amino acid sequence of HF-COLL-18/514cf.

USE - Medicaments containing HF-COLL-18/514cf or its derivatives or fragments are useful for treating human diseases, especially involving supporting or connective tissue, the respiratory or urogenital tract, the cardiovascular or nervous system, the integuments or the sense organs. The medicaments are also used for treating systemic diseases with overproduction or deficiency of HF-COLL-18/514cf, especially with e.g. use of antibodies raised against this or HF-COLL-18/514cf for substitution therapy. The protein, in a suitable form, can also be used to treat chronic diseases involving electrolyte action in diseases on the bone reconstruction (osteoporosis) or at the dental apparatus. The protein is also used for diagnosis of diseases by producing specific antibodies against synthetic fragments or the entire peptide or its derivatives and its fragments and measuring the blood concentration of HF-COLL-18/514cf via an immunoassay.

Dwg.0/0

FS CPI EPI

FA AB; DCN

MC CPI: B04-N02; B14-F01B; B14-J01; B14-K01; B14-N07C; D05-H09; D05-H11; D05-H17A6
EPI: **S03-E14H4**

L54 ANSWER 12 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

AN 1997-274921 [25] WPIDS

DNN N1997-227696 DNC C1997-088519

TI **Structural analysis** of analyte ions using a time-of-flight mass spectrometer - involves analyte ions entering fragmentation zone as divergent ion beam, after which an Einzel lens focusses spontaneously decaying ions onto an ion detector as opposed to metastable daughter ions.

DC B04 J04 S03 V05

IN KOESTER, C

PA (BRUK-N) BRUKER FRANZEN ANALYTIK GMBH

CYC 3

PI GB 2307782 A 19970604 (199725)* 15p H01J049-00
DE 19544808 A1 19970605 (199728) 8p H01J049-46
US 5734161 A 19980331 (199820) 8p H01J049-40

ADT GB 2307782 A GB 1996-24948 19961129; DE 19544808 A1 DE 1995-19544808 19951201; US 5734161 A US 1996-757895 19961127

PRAI DE 1995-19544808 19951201

IC ICM H01J049-00; H01J049-40; H01J049-46
ICS G01N027-62; **G01N033-68**

AB GB 2307782 A UPAB: 19970619

The structural analysis of analyte ions using a time-of-flight **mass spectrometer** involves measuring daughter ions which are generated from a beam of analyte ions in a fragmentation zone (19) by high-energy collisions with gas molecules.

The method involves: (a) causing the analyte ions to enter the fragmentation zone as a divergent ion beam, which is not focused onto the ion detector, and (b) providing an Einzel lens (4-6) adjacent the fragmentation zone to focus the spontaneously decaying ions, which have lower kinetic energies than the unfragmented ions, onto the ion detector, in order to favour detection of daughter ions formed by spontaneous decay, as compared with daughter ions formed by metastable decay taking place at a later stage in the **mass spectrometer.**

Also claimed is an appts. for performing the above method.

USE - For the structural analysis of large molecules e.g. chain molecules such as peptides and proteins.

ADVANTAGE - Enables spontaneously generated daughter ions and delayed metastable resulting daughter ions to be measured separately thus enabling recognition and measurement of e.g. D and W (i.e. N-terminal and C-terminal) ions, and enables measurement of even granddaughter ions from spontaneously formed daughter ions without interference, due to use of e.g. electrostatic energy filtration using a short Einzel lens directly behind the collision zone to differentiate between spontaneous and delayed ion fragmentation. Enables e.g. determn. of whether a terminal amino acid is leucine or isoleucine, even though they both has the same **mass** , because their D-ions have different **masses.**

PREFERRED METHOD - A time-of-flight **mass spectrometer** with a **matrix-assisted laser** (8) **desorption** and **ionisation** (**MALDI**) ion source is used. The divergence of the ion beam is generated by the effect of the lateral velocities gained by the ions (12) in the **MALDI** process. An ion source (1-3) with grid-less apertures (10,11) is employed. The appts. includes an ion reflector to analyze the energy of ions, and thus scan the daughter ion spectra. The electric acceleration field in front of the sample support (1) can be switched on with a time delay relative to the **laser** light flash of the **MALDI** ion source. The fragmentation zone is a collision cell filled with a collision gas cloud (19) having a pressure of from 10-3 to 10-1 millibars, formed in the vacuum system of the **mass spectrometer** in front of a gas supply nozzle(17), which supplies gas in pulses.

In subsequently acquired daughter ion spectra, spontaneously fragmented and unfragmented ions are measured by the detector in an alternating fashion, thus distinguishing spontaneously generated daughter ions from ions generated by metastable decay, the alternating measurements being obtained by changes of the focusing voltage at the Einzel lens and/or by changes of the supply of collision gas. Daughter ions of relatively low kinetic energy generated by spontaneously decay, are discriminated from daughter ions of relatively high kinetic energy generated by metastable decay.

Dwg.1/2

FS CPI EPI
FA AB; GI
MC CPI: B04-N04; B11-C08A; B12-K04; J04-B01A
EPI: S03-E10A3; S03-E14H5; V05-J01A1; V05-J01G

L54 ANSWER 13 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1995-246393 [32] WPIDS
CR 1995-241503 [32]
DNN N1995-191319 DNC C1995-113090
TI New human circulating cytokine CC-1 and related nucleic acid - used to treat abnormal cell migration, tumours etc. also diagnostically isolated from haemofiltrate.
DC B04 D16 S03
IN **FORSSMANN, W**; MAGERT, H; MEYER, M; **SCHULZ-KNAPPE, P**; MAEGERT, H
PA (FORS-I) FORSSMANN W

CYC 60
PI WO 9518228 A1 19950706 (199532)* DE 25p C12N015-19
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ
W: AM AU BB BG BR BY CA CN CZ EE FI GE HU JP KG KP KR KZ LK LR LT LV
MD MG MN NO NZ PL RO RU SI SK TJ TT UA US UZ VN
AU 9513849 A 19950717 (199544) C12N015-19
DE 4427395 A1 19960208 (199611) 12p C07K014-00
EP 736095 A1 19961009 (199645) DE C12N015-19
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
AU 680714 B 19970807 (199740) C12N015-19
JP 09510084 W 19971014 (199751) 22p C12N015-09
ADT WO 9518228 A1 WO 1994-EP4282 19941222; AU 9513849 A AU 1995-13849 19941222; DE 4427395 A1 DE 1994-4427395 19940803; EP 736095 A1 WO 1994-EP4282 19941222, EP 1995-905105 19941222; AU 680714 B AU 1995-13849 19941222; JP 09510084 W WO 1994-EP4282 19941222, JP 1995-517774 19941222
FDT AU 9513849 A Based on WO 9518228; EP 736095 A1 Based on WO 9518228; AU 680714 B Previous Publ. AU 9513849, Based on WO 9518228; JP 09510084 W Based on WO 9518228
PRAI DE 1994-4427395 19940803; DE 1993-4344397 19931224
REP 1.Jnl.Ref; WO 9313206
IC ICM C07K014-00; C12N015-09; C12N015-19
ICS A61K038-00; A61K038-19; A61K049-00; C07H021-04; C07K001-18; C07K001-20; C07K001-30; C07K014-52; C12P021-02; C12P021-08; C12Q001-68; G01N033-53; **G01N033-68**
AB WO 9518228 A UPAB: 19950818
Cytokine CC-1 of formula (I) is new. Also included are its fragments and/or derivs., esp. amidated, acetylated, phosphorylated and/or glycosylated derivs. TKTESSSRGPYHPSECCFTYTTYKIPRQRIMDYYETNSQCSKPGIVFITKRGH SVCTNPSDKWVQDYIKDMKEN (I) Also new are: (1) polynucleotides (II) encoding (I) or its fragments, (2) poly- or monoclonal antibodies specific for (II) or the cytokine CC-1 mRNA, and (3) probes (III) that hybridise with (II). A cDNA of 123 bp encoding part of (I) is reproduced in the specification.
USE - (I) is useful for treating diseases involving abnormal cell migration, immune system diseases, tumours and aberrations of regulatory growth functions (claimed). (II) and its fragments can be used to express recombinant (I) or to detect (I)-encoding nucleic acid. Antibodies raised against (I) can be used diagnostically in usual ELISA or RIA.
Dwg.0/4
FS CPI EPI
FA AB; DCN
MC CPI: B04-E02B; B04-E05; B04-H01; B11-C08E5; B12-K04A; B12-K04F; B14-H01B; D05-H09; D05-H11; D05-H12A; D05-H12D1
EPI: **S03-E14H4**

L54 ANSWER 14 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1994-178855 [22] WPIDS
DNN N1994-140821 DNC C1994-081691
TI **Low mol. wt.** reducing agent for met-myoglobin - comprises nonionic material of molecular weight 1000 to 3000 and optimum redn. pH about 6.
DC B04 D16 S03
PA (NAMI-I) NAMIKI H
CYC 1
PI JP 06118087 A 19940428 (199422)* 7p G01N033-68 <--
ADT JP 06118087 A JP 1992-267251 19921006
PRAI JP 1992-267251 19921006
IC ICM **G01N033-68**
AB JP 06118087 A UPAB: 19940722
Reducing agent for metmyoglobin is non-anionic material of mol. wt. 1000-3000 and optimum redn pH about 6.
The reducing agent is obtd. from e.g. bovine myocardium. The myocardium is extracted, the extract liq. is fractionated by ultrafiltration and then liq. chromatography. The reducing agent has **low molecular weight** (1000-3000), consequently the reducing agent is easily discharged into blood, which is effective for the determn. of metmyoglobin-reductase in muscular tissue.

USE/ADVANTAGE - By determining concn. of the reducing agent of metmyoglobin in blood or urine, the amt. of metmyoglobin reductase in muscular tissue is easily detected, consequently the diagnosis of motility load, alcoholism, carbon monoxide poisoning etc. is carried out.

In an example, the reducing agent of metmyoglobin was prepd from bovine myocardium. The reducing agent exhibited high reducing power (high diaphorase activity).

Dwg.1/5

FS CPI EPI
FA AB; GI
MC CPI: B04-B04B1; B04-B04D5; B04-B04H; B04-L03D; B11-C08E3; B12-K04A; D05-H09
EPI: S03-E14H5

L54 ANSWER 15 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1993-351872 [44] WPIDS
DNN N1993-271377 DNC C1993-156239
TI Detection of nitric oxide, S-nitroso-thiol cpds. and S-nitroso-proteins - by photolysis and measuring chemiluminescence after reaction with ozone.
DC B04 S03
IN LOSCALZO, J; STAMLER, J
PA (BGHM) BRIGHAM & WOMENS HOSPITAL
CYC 21
PI WO 9321525 A1 19931028 (199344)* EN 28p G01N033-00
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: AU CA JP
AU 9341114 A 19931118 (199410) G01N033-00
EP 591511 A1 19940413 (199415) EN G01N033-00
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
JP 06510605 W 19941124 (199506) 9p G01N021-76
EP 591511 A4 19940817 (199533) G01N033-00
US 5459076 A 19951017 (199547) 11p G01N033-00
AU 664276 B 19951109 (199601) G01N033-68 <--
EP 591511 B1 19980204 (199810) EN 13p G01N021-63
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
DE 69316818 E 19980312 (199816) G01N021-63
ES 2114049 T3 19980516 (199826) G01N021-63
ADT WO 9321525 A1 WO 1993-US3785 19930421; AU 9341114 A AU 1993-41114 19930421; EP 591511 A1 EP 1993-910720 19930421, WO 1993-US3785 19930421; JP 06510605 W JP 1993-517831 19930421, WO 1993-US3785 19930421; EP 591511 A4 EP 1993-910720 ; US 5459076 A US 1992-872237 19920422; AU 664276 B AU 1993-41114 19930421; EP 591511 B1 EP 1993-910720 19930421, WO 1993-US3785 19930421; DE 69316818 E DE 1993-616818 19930421, EP 1993-910720 19930421, WO 1993-US3785 19930421; ES 2114049 T3 EP 1993-910720 19930421
FDT AU 9341114 A Based on WO 9321525; EP 591511 A1 Based on WO 9321525; JP 06510605 W Based on WO 9321525; AU 664276 B Previous Publ. AU 9341114, Based on WO 9321525; EP 591511 B1 Based on WO 9321525; DE 69316818 E Based on EP 591511, Based on WO 9321525; ES 2114049 T3 Based on EP 591511
PRAI US 1992-872237 19920422
REP 1.Jnl.Ref; US 3967933; US 3973910; US 4368262; US 5094815; 2.Jnl.Ref; SU 1464084; US 4272248; US 4775633
IC G01N033-48
ICM G01N021-63; G01N021-76; G01N033-00; **G01N033-68**
ICS G01N030-74; G01N033-48; G01N033-52
AB WO 9321525 A UPAB: 19931213
(A) A method for detecting **low mol. wt.** S-nitrosothiols in a biological fluid sample is claimed, which comprises: (a) subjecting the sample to photolysis; (b) quantitating the amt. of nitric oxide (NO) in the sample by measuring the chemiluminescence signal (CLS) generated by a chemical reaction between NO and ozone; (c) inactivating the CLS-generating capability of any NO which is associated with a thiol in a separate sample of the biological fluid, e.g. by treatment with mercurous ion; (d) detecting the NO in the sample obtd. in step (c) using steps (a) and (b) and (e) determining the quantitative difference between the amt. of NO detected in steps (b) and (d) to

determine the amt. of S-nitrosothiols in the sample.

USE/ADVANTAGE - The method can be used for the sensitive detection of NO and permits its distinction from nitric oxide equivalents. The method can be used to detect and monitor disease states involving abnormal levels of nitric oxide and nitrosonium equivalents. It can be used to monitor septic shock, cardiogenic shock, hypovolemic shock, atherosclerosis, hyperhomocysteinemia, venous thrombosis, arterial thrombosis, coronary occlusion, pulmonary embolism, cerebrovascular accident, vascular fibrosis, ectopia lentis, osteoporosis, mental retardation, skeletal deformities, pulmonary hypertension, malignancy, infection and central nervous system disorders.

Dwg.1/3

FS CPI EPI

FA AB; GI; DCN

MC CPI: B04-B04D5; B05-C08; B10-A03; B12-K04A
EPI: S03-E04E; S03-E14H

ABEQ US 5459076 A UPAB: 19951128

S-nitrosothiols in a biological fluid sample are detected, by (a) subjecting sample to photolysis; (b) measuring the amt. of NO present from the chemi-luminescence signal generated from the reaction between NO and O3; (c) inactivating chemiluminescence signal-generating capability of NO associated with thiol in a separate sample of fluid; (d) detecting NO in (c) using steps (a) and (b); and (e) determining the quantitative difference between NO detected in (b) and (d) to determine the amt. of S-nitrosothiol in the sample.

Pref., thiol is inactivated by treating sample with a mercurous ion.

USE - Used for monitoring NO bioactivity in normal physiological state and disease state, e.g., septic shock, atherosclerosis, thrombosis, hyperhomocysteinaemia, pulmonary hypertension, malignancy, infection, and CNS disorders.

Dwg.1/3

ABEQ EP 591511 B UPAB: 19980309

(A) A method for detecting **low mol. wt.**

S-nitrosothiols in a biological fluid sample is claimed, which comprises: (a) subjecting the sample to photolysis; (b) quantitating the amt. of nitric oxide (NO) in the sample by measuring the chemiluminescence signal (CLS) generated by a chemical reaction between NO and ozone; (c) inactivating the CLS-generating capability of any NO which is associated with a thiol in a separate sample of the biological fluid, e.g. by treatment with mercurous ion; (d) detecting the NO in the sample obtd. in step (c) using steps (a) and (b) and (e) determining the quantitative difference between the amt. of NO detected in steps (b) and (d) to determine the amt. of S-nitrosothiols in the sample.

USE/ADVANTAGE - The method can be used for the sensitive detection of NO and permits its distinction from nitric oxide equivalents. The method can be used to detect and monitor disease states involving abnormal levels of nitric oxide and nitrosonium equivalents. It can be used to monitor septic shock, cardiogenic shock, hypovolemic shock, atherosclerosis, hyperhomocysteinemia, venous thrombosis, arterial thrombosis, coronary occlusion, pulmonary embolism, cerebrovascular accident, vascular fibrosis, ectopia lentis, osteoporosis, mental retardation, skeletal deformities, pulmonary hypertension, malignancy, infection and central nervous system disorders.

Dwg.1/3

L54 ANSWER 16 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

AN 1986-305118 [46] WPIDS

DNN N1986-228056 DNC C1986-132293

TI **Mol. wt.** determn. of proteins - using **immunoglobulin** components as **mol. wt.** markers.

DC A89 B04 J04 **S03**

IN HEARN, M T W; MARLEY, P B

PA (COMU) CIE FR MATERIEL COLORANTES; (COMW) COMMONWEALTH SERUM LAB COMMISS; (DAVI-I) DAVIES J R

CYC 17

PI WO 8606383 A 19861106 (198646)* EN 20p

RW: AT BE CH DE FR GB IT LU NL SE
W: DK JP NO US
AU 8656888 A 19861106 (198651)
NO 8605333 A 19870302 (198715)
EP 221116 A 19870513 (198719) EN
R: AT BE CH DE FR GB IT LI LU NL SE
DK 8606344 A 19870302 (198751)
JP 63500207 W 19880121 (198809)
CA 1272938 A 19900821 (199039)
ADT WO 8606383 A WO 1986-AU118 19860430; EP 221116 A EP 1986-902779 19860430; JP 63500207 W JP 1986-502591 19860430
PRAI AU 1985-381 19850501; AU 1986-56888 19860430
REP 7.Jnl.Ref; AU 8319345; DE 3018901; EP 131836; SSR871104; US 4107014; US 4347179
IC C07K015-12; **G01N033-68**
AB WO 8606383 A UPAB: 19930922
Compns. (I) for use in the detern. of the **mol. wt.** of proteins comprises at least one protein or polypeptide of known **mol. wt.** selected from the gp. of Ig components consisting of the immuno-globulins, fragments and their polymers.
Also claimed is a method for detection and/or determination of the **mol. wts.** of one or more sample proteins comprising (a) simultaneously subjecting the sample proteins and (I) to electrophoretic resolution on a polymeric gel; and (b) detecting and comparing the resolved sample proteins and Ig components in order to detect or determine the **mol. wts.** of the sample proteins.
ADVANTAGE - The new **mol. wt.** markers can be detected on all supports. Detection of **mol. wt.** markers and sample protein is simultaneous and onlyone procedure is required. Detection of marker does not require the removal of lanes contg. the markers from the rest of the support.
0
FS CPI EPI
FA AB
MC CPI: A03-C01; A04-D04A1; A10-E12A; A12-L04; A12-S; A12-V03C2; **B04-B04A**; B04-B04C6; B04-C01; B11-C08D1; B12-K04E; J04-B01B
EPI: **S03-E14H4**

L54 ANSWER 17 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD
AN 1985-171361 [28] WPIDS
DNN N1985-128894 DNC C1985-074955
TI New peptide hormone cardiodilatine - from atrium tissue having effects on heart muscle ionotropy, smooth muscle, and sweat secretion.
DC B04 S03
IN **FORSSMANN, W; FORSSMANN, W G**
PA (FORS-I) FORSSMANN W; (FORS-I) FORSSMANN W-G; (ORGA-N) ORGANOGEN MED MOL; (FORS-I) FORSMAN W G
CYC 12
PI WO 8502850 A 19850704 (198528)* DE 35p
RW: AT BE CH DE FR GB LU NL SE
W: JP US
DE 3346953 A 19850814 (198534)
EP 167575 A 19860115 (198603) DE
R: AT BE CH DE FR GB LI LU NL SE
JP 61500848 W 19860501 (198624)
US 4751284 A 19880614 (198826)
US 4782044 A 19881101 (198846)
US 4895932 A 19900123 (199011)
EP 167575 B1 19930526 (199321) DE 10p C07K007-10
R: AT BE CH DE FR GB LI LU NL SE
DE 3346953 C2 19930603 (199322) 5p C07K015-06
DE 3486154 G 19930701 (199327) C07K007-10
JP 07072146 A 19950317 (199520) 10p G01N033-53
JP 08022876 B2 19960306 (199614) 16p C07K014-58
JP 08224094 A 19960903 (199645) 9p C12P021-06
EP 167575 B2 19991027 (199950) DE C07K014-58

R: AT BE CH DE FR GB LI LU NL SE

ADT WO 8502850 A WO 1984-DE279 19841221; DE 3346953 A DE 1983-3346953 19831224; EP 167575 A EP 1985-900447 19841221; JP 61500848 W JP 1985-500395 19841221; US 4751284 A US 1985-769627 19850820; US 4782044 A US 1988-140736 19880104; US 4895932 A US 1988-229706 19880808; EP 167575 B1 WO 1984-DE279 19841221, EP 1985-900447 19841221; DE 3346953 C2 DE 1983-3346953 19831224; DE 3486154 G DE 1984-3486154 19841221, WO 1984-DE279 19841221, EP 1985-900447 19841221; JP 07072146 A Div ex JP 1985-500395 19841221, JP 1994-2150 19841221; JP 08022876 B2 WO 1984-DE279 19841221, JP 1985-500395 19841221; JP 08224094 A Div ex JP 1985-500395 19841221, JP 1995-260453 19841221; EP 167575 B2 WO 1984-DE279 19841221, EP 1985-900447 19841221

FDT EP 167575 B1 Based on WO 8502850; DE 3486154 G Based on EP 167575, Based on WO 8502850; JP 08022876 B2 Based on JP 61500848, Based on WO 8502850; EP 167575 B2 Based on WO 8502850

PRAI DE 1983-3346953 19831224

REP 2.Jnl.Ref; 3.Jnl.Ref

IC A61K035-34; A61K037-02; A61K049-00; C07K007-10; C07K015-12; **G01N033-68**

ICM C07K007-10; C07K014-58; C07K015-06; C12P021-06; G01N033-53

ICS A61K035-34; A61K037-02; A61K038-17; A61K049-00; C07K007-06; C07K007-08; C07K015-12; **G01N033-68**

ICA A61K038-00; A61K038-22; A61K039-395; C07K016-26

AB WO 8502850 A UPAB: 19950518

Peptide hormone cardiodilation has the N-terminal amino acid sequence: Asn-Pro-Val-Try-Gly-Ser-Val-Ser-Asn -Ala-Asp-Leu-Met-Asp-Phe-Lys-Asn-Leu -Leu-Asp-His-Leu-Glu-Asa-Lys-Met-Pro -Leu-Glu-Asp-Glu-Ala-Met-Pro-Pro-Gln -Val-Leu-Ser-Glu-Gln-Asp-Glu-Val-Leu -Ser-Glu-Gln-Asn-Glu-Glu-Val-Gly-Ala -Pro-Leu-Pro-Leu-Leu-Glu-Glu-Val-Pro -Pro-Trp-Thr-Gly-Glu-Val-Asn-Pro; and the composition Asp/Asn 14, Thr 3, Ser 15, Glu/Gln 12, Pro 10, Gly 12, Ala 10, Val 7, Met 4, Ile 1, Leu 15, Tyr 2, Phe 3, Lys 4, His 2, Arg 10, Trp 2. It has an isoelectric point of 6-6.5.

USE - The new peptide hormone and its active fragments have effect on the ionotropy of heart muscle, as well as effects on vascular smooth muscle and on sweat secretion and can be used clinically and therapeutically particularly in the diagnosis and therapy of hypertension. They can also be used for the treatment of post-operative cardiovascular disorders, skin diseases, involving disorders of sweat secretion, cardiovascular shock, renal and adrenal disorders, and digestive tract disorders.

Dwg.0/9

Dwg.0/9

FS CPI EPI

FA AB

MC CPI: B04-C01; B12-F02; B12-G03; B12-G04; B12-J01; B12-L01

EPI: **S03-E14H9**

ABEQ US 4751284 A UPAB: 19930925

A virtually pure peptide hormone cardiodilatin has an isoelectric point 6-6.5, an amino acid content Asp/Asn 14, Thr 3, Ser 15, Glu/Gln 12, Pro 10, Gly 12, Ala 10, Val 7, Met 4, Ile 1, Leu 15, Tyr 2, Phe 3, Lys4, His 2, Arg 10 and Trp 2, and an N-terminal amino acid sequence Asn-Pro-Val-Tyr-Gly-Ser-Val-Ser- Asn-Ala-Asp-Leu- Met-Asp-Phe-Lys-Asn-Leu-Leu-Asp- His-Leu-Glu-Asp- Lys-Met-Pro-Leu- Glu-Asp-Glu-Ala-Met-Pro-Pro-Gln-Val-Leu-Ser-Glu- Gln-Asp-Glu-Glu-Val-Gly-Ala-Pro -Leu-Pro-Leu-Leu -Glu-Glu-Val-Pro -Pro-Trp-Thr-Gly-Glu-Val-Asn-Pr.

Biologically active fragments of cardiodilatin are pref. included, esp. fragments terminating at but not including a Met or Arg residue at at least 1 end. The C-terminal fractions are suitably obtd. after partial cyanogen bromide fission between and behind Met gps.

USE/ADVANTAGE - For diagnosis and therapy of hypertonia; the peptide (fragments) has a high relaxing action on the smooth blood vessel muscles.

ABEQ US 4782044 A UPAB: 19930925

Compsn. for treating a disease involving irregularities in tension or dilation of blood vessels comprises an ionotropic pure peptide hormone cardiodilatin or a fragemnt of it. The cardiodilatin has isoelectric point 6-6.5, 126 amino acid residues and an amino acid compsn. of Asp/Asn 14,

Thr 3, Ser 15, Glu/Gln 12, Pro 10, Gly ,2, Ala 10, Val 7, Met 4, Ile 1, Leu 15, Tyr 2, Phe 3, Lys 4, His 2, Arg 10 and Trp 2.

USE - The compsn. may be adminstered orally or parenterally and pref. comprises 10-1000 ng cardiodilatin or its fragment per dosage unit. The hormone may abo be used diagnastically.

ABEQ US 4895932 A UPAB: 19930925

Determn. of cardiodilatin (I) or its fragment utilises a new antibody produced in response to immunisation of a host with (I) or fragments of specified amino acid sequence. A body fluid sample is contacted with the antibody which specifically binds to (I) or its fragment and binding is determined.

The antibody may be radiolabelled or enzymatically labelled. The antibody is claimed per se.

USE - In hypertonia diagnosis and therapy.

ABEQ EP 167575 B UPAB: 19931114

The peptide hormone cardiodilatin having the N-terminal amino acid sequence Asn-Pro-Val-Tyr-Gly-Ser-Val -Ser-Asn-Ala-Asp-Leu-Met -Asp-Phe-Lys-Asn-Leu-Leu -Asp-His-Leu-Glu-Asp-Lys-Met -Pro-Leu-Glu-Asp-Glu-Ala- -Met-Pro-Pro-Gln-Val-Leu -Ser-Glu-Gln-Asp-Glu, wherein arginine moieties are present also in the subsequent amino acid sequence, and/or its biologically active fragments, obtainable in the form of active fractions, starting from atrium extract by fractionating a material extractable with aqueous solvents in accordance with conventional biochemical purification methods, using an assay wherein the active fractions are determined by the relaxant effect onto the smooth musculature.

Dwg.0/1

ABEQ DE 3346953 C UPAB: 19931115

Peptide hormone cardiodilatin has an N-terminal sequence of formula Asn-Pro-Val-Tyr-Gly-Ser-Val-Ser -Asn-Ala-Asp-Leu-Met-Asp-Leu-Met-Asp-Phe-Lys -Asn-Leu-Leu-Asp-His-Leu-Glu-Asp -Lys-Met-Pro-Leu-Glu-Asp -Glu-Ala-Met-Pro-Pro-Gln-Val -Leu-Ser-Glu-Gln-Asp-Glu... Prepn. of cardiodilatin and/or its biologically active fragments (adjacent to Met and/or Arg gps). comprises fractionation of the aq. extracts from procine atrium tissues and the usual biochemical purificn. methods, monitoring the active components by their relaxing activity on smmoth muscle tissues.

USE - The prods. are diagnostic agents and therapeutics for hypertonia. Dosage is 10-1000ng.

Dwg.1/1

L54 ANSWER 18 OF 18 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

AN 1985-108192 [18] WPIDS

DNN N1985-081066 DNC C1985-046945

TI **Low mol. wt.** peptide **immobilisation** - in carrier gel using formaldehyde **vapour.**

DC A96 B04 D16

PA (HITA) HITACHI LTD

CYC 1

PI JP 60052758 A 19850326 (198518)* 4p

ADT JP 60052758 A JP 1983-160343 19830902

PRAI JP 1983-160343 19830902

IC G01N027-26; **G01N033-68**

AB JP 60052758 A UPAB: 19930925

The **low mol. wt.** peptide is immobilised by using the vapour of formaldehyde, polyvalent aldehyde or polyvalent isocyanate. Protein and peptide, esp. **low mol. wt.** peptide of about several 1000 mol. wt. can be surely immobilised in a carrier gel for electrophoresis, which makes it possible to detect **low mol. wt.** peptide. The method is esp. useful for e.g. the examination of urine, etc.

The immobilising reagent used in the invention is e.g. formaldehyde, glutaraldehyde, paraformaldehyde, hexamethylene diisocyanate, tolylene diisocyanate, etc. The reaction with the reagent is carried out at room temp. under normal pressure when the reagent has high vapour pressure at normal temp. or by heat under reduced pressure when it has low vapour pressure at normal temp.

Carrier gel used is e.g. polyacrylamide gel. The detection of protein (**low mol. wt.** peptide) in polyacrylamide gel can be sensitively and rapidly carried out.

In the previous method, protein in a carrier gel is pptd. and immobilised by a buffer liq. contg. 50% methanol and detected by using a dye. In this method, **low mol. wt.** peptide is not thoroughly immobilised and flows out of the carrier gel. In the new method, **low mol. wt.** peptide is surely immobilised and the detection of the peptide is carried out by measuring the fluorescence. Tryptophane gp. of protein immobilised in the carrier gel is oxidised by hydrogen peroxide-dioxan and treated with acid to form kynurenine exhibiting a strong fluorescence at about 120 nm, and the protein spot in the carrier gel can be detected by measuring the fluorescence.

0/0

FS CPI
FA AB
MC CPI: A12-V03C; **B04-B04A**; B04-B04B; B04-C01; B04-C03B; B11-C07B; B12-K04; D05-H

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=> fil biosis
FILE 'BIOSIS' ENTERED AT 09:07:02 ON 30 DEC 1999
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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 29 December 1999 (19991229/ED)

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for details.

=> d his l57-

     (FILE 'WPIDS' ENTERED AT 07:28:06 ON 30 DEC 1999)

     FILE 'WPIDS' ENTERED AT 08:23:35 ON 30 DEC 1999

     FILE 'BIOSIS' ENTERED AT 08:24:31 ON 30 DEC 1999
L57         3015 S ?MALDI? OR MATRIX (L) ASSIS? (L) LASER? (L) ?SPECTROM?
L58         2859 S ?MALDI? OR MATRIX (L) ASSIS? (L) LASER? (L) DESORPT? (L) IONI
L59         3000 S ?MALDI? OR MATRIX (L) ASSIS? (L) LASER? (L) DESORPT? (L) MASS
L60         2863 S ?MALDI? OR MATRIX (L) ASSIS? (L) LASER? (L) IONI? (L) MASS (L
L61         3015 S L57-L60
L62          828 S L61 AND ?PEPTIDE?
L63         1142 S L61 AND (10054 OR 10064)/CC
L64         1438 S L62,L63
L65          174 S L64 AND (?ELECTROSPRAY? OR ?ELECTRO SPRAY?)
L66          459 S L64 AND ?CHROMATOG?
L67           88 S L65 AND L66
L68           19 S L67 AND MOLECULAR WEIGHT
L69          358 S L66 AND (10502 OR 10504 OR 10050)/CC
L70          348 S L66 AND (*10502 OR *10504 OR *10050)/CC
L71           10 S L69 NOT L70
                E MISCELLANEOUS/IT
L72       164572 S E3 (L) DESCRIPTOR#/IT (L) (ANALYTICAL METHOD)
L73           80 S L70 AND L72
L74           12 S L73 AND (MICROMETHOD# OR GEL OR LYMPHOCYTE OR ENGINEER? OR CO
L75          268 S L70 NOT L73
L76          223 S L75 NOT (10058 OR 10068 OR 10052 OR 10062)/CC
L77            2 S L76 AND (ANALYSIS AND SYNTHETIC)/TI
L78            1 S L77 NOT TOXINS/TI
L79           64 S L76 AND (MICROBORE OR MAP? OR DEVELOPMENT OR BACTERIAL OR COU
L80            2 S L76 AND (LASER DESORPTION MASS SPECTROMETRY)/TI
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L81           1 S L80 NOT CFTR/TI
L82          43 S L79 NOT (HEVEIN OR RENAL OR SIGNAL OR MYELOID OR CLEAVAGE OR
L83          31 S L82 NOT (TYROSIN? OR ENZYM? OR CHINESE OR TRANSFERRIN OR KINA
L84          25 S L83 NOT (TANDEM OR PNA OR COLI OR THROMBIN OR BLEOMYCIN OR AC
L85          39 S L74,L78,L81,L84
                E FORSSMAN/AU
L86         546 S E14,E15,E25-E32
                E SCHULZ KNAP/AU
L87          55 S E4-E6
                E SCHRADER M/AU
L88         106 S E3-E9,E18,E19
                E OPITZ H/AU
L89          93 S E3,E4,E9
L90         740 S L86-L89
L91           3 S L90 AND L85
L92          36 S L85 NOT L91

     FILE 'BIOSIS' ENTERED AT 09:07:02 ON 30 DEC 1999

=> d all tot

L92  ANSWER 1 OF 36  BIOSIS  COPYRIGHT 1999 BIOSIS
AN   2000:13994  BIOSIS
DN   PREV200000013994
TI   A novel interface for on-line coupling of liquid capillary
     chromatography with matrix-assisted laser desorption/ionization
     detection.
AU   Zhan, Qiao; Gusev, Arkady; Hercules, David M. (1)
CS   (1) Department of Chemistry, Vanderbilt University, Station B, Nashville,
     TN, 37235 USA
SO   Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 22, pp.
     2278-2283.
     ISSN: 0951-4198.
DT   Article
LA   English
SL   English
AB   A novel interface has been developed which should allow the direct on-line
     coupling of liquid capillary chromatography with matrix
     -assisted laser desorption/
     ionization (MALDI) mass spectrometry
     detection. The interface employs continuous analyte/matrix
     co-crystallization onto a porous frit installed at a capillary end which
     is used as the target for MALDI. After separation, the analyte
     effluent is premixed with the MALDI matrix solution
     and introduced into the interface. The analyte/matrix mixture is
     co-crystallized onto the frit surface in the vacuum environment of the
     mass spectrometer. Continuous matrix/analyte
     crystallization and interface regeneration is accomplished by a
     combination of solvent flushing and laser ablation. The memory
     effect is negligible over a dynamic range of ca. 200. Several
     applications, including analysis of small peptides and
     combination with gel permeation chromatography (GPC), have
     indicated that the on-line MALDI interface does not sacrifice
     chromatograph ic or mass spectral resolution, and have
     demonstrated the possibility of a reliable LC-MALDI system.
CC   Biochemical Studies - General  *10060
       Biochemical Methods - General  *10050
       Biophysics - General Biophysical Studies  *10502
     Endocrine System - General  *17002
IT   Major Concepts
       Biochemistry and Molecular Biophysics; Methods and Techniques
IT   Chemicals & Biochemicals
       angiotensin II: Sigma, analysis; bradykinin: Sigma, analysis
IT   Methods & Equipment
       GPC instrument: equipment; HPLC instrument: equipment; gel permeation
       chromatography [GPC]: chromatographic techniques,
```

separation method; high performance liquid **chromatography**: liquid **chromatography**, on-line coupling interface, separation method; **matrix-assisted laser/ desorption ionization-mass spectrometry** [**MALDI**-MS]: analytical method, spectroscopic techniques: CB; modified LAMMA 1000 reflectron time-of-flight **laser mass spectrometer**: equipment

RN 11128-99-7 (ANGIOTENSIN II)
58-82-2 (BRADYKININ)

L92 ANSWER 2 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:507927 BIOSIS
DN PREV199900507927
TI **Identification** of proteins from two-dimensional gel electrophoresis of human erythroleukemia cells using capillary high performance liquid **chromatography**/electrospray-ion trap-reflectron time-of-flight mass spectrometry with two-dimensional topographic **map** analysis of in-gel tryptic digest products.
AU Chen, Yajuan; Jin, Xiaoying; Misek, David; Hinderer, Robert; Hanash, Sam M.; Lubman, David M. (1)
CS (1) Department of Chemistry, The University of Michigan, Ann Arbor, MI, 48109-1055 USA
SO Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 19, pp. 1907-1916.
ISSN: 0951-4198.
DT Article
LA English
SL English
AB Protein spots from two-dimensional (2-D) gel electrophoresis of a human erythroleukemia cell line have been identified by analysis of the in-gel tryptic digests using capillary high performance liquid **chromatography** (HPLC) separation with on-line detection using electrospray **ionization mass spectrometry** (ESI-MS). This is performed using an electrospray/ion trap storage/reflectron time-of-flight **mass spectrometer** system (ESI-IT-reTOFMS). A 2-D topographic mapping display developed to process the on-line data acquired with this TOF system has been used to obtain **mass** identification of each **peptide**, even though the capillary HPLC only provides limited separation capability of the tryptic **peptide** mixtures studies herein. Using this method, a substantial fraction of the protein sequence can be covered and identified using the tryptic map. It is demonstrated that by entering the cell species, the approximate MW and pI range as determined by 2-D gel electrophoresis, and the tryptic **peptide** map into the database a unique match for identification of the protein generally results. It is also demonstrated that a much improved coverage of the protein sequence is obtained by this method relative to **matrix-assisted laser desorption/ionization mass spectrometry** (**MALDI**-MS).
CC Cytology and Cytochemistry - Human *02508
Biochemical Methods - General *10050
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Methods and Techniques
IT Parts, Structures, & Systems of Organisms
human erythroleukemia cells
IT Chemicals & Biochemicals
proteins: analysis, identification, in-gel tryptic digest products
IT Methods & Equipment
capillary high performance liquid **chromatography**: **chromatographic** techniques, separation method; electrospray ion-trap reflectron time-of-flight mass spectrometry [ESI-IT-reTOFMS]: analytical method, spectroscopic techniques: CB; ion-trap reflectron

time-of-flight mass spectrometer: Jordan Co., equipment; two-dimensional gel electrophoresis: polyacrylamide gel electrophoresis, separation method; two-dimensional topographic map analysis: Analysis/Characterization Techniques: CB, analytical method; HPLC instrument: equipment

L92 ANSWER 3 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:438057 BIOSIS
DN PREV199900438057
TI **Rapid** screening of protein profiles of human **breast** cancer cell lines using non-porous reversed-phase high performance liquid **chromatography** separation with matrix-assisted laser desorption/ionization time-of-flight mass spectral analysis.
AU Chong, Bathsheba E.; Lubman, David M. (1); Miller, Fred R.; Rosenspire, Allen J.
CS (1) Department of Chemistry, University of Michigan, Ann Arbor, MI, 48109-1055 USA
SO Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 18, pp. 1808-1812.
ISSN: 0951-4198.
DT Article
LA English
SL English
AB Non-porous reversed-phase (NP-RP) HPLC has been used to rapidly generate protein profiles of whole cell lysates of human breast cancer cell lines. The non-porous packing material used was silica coated with C18, which provided rapid separation with high collection efficiency of proteins from cell lysates. This method was used to study the differences in protein profiles among normal cells and fully malignant cells that share a common genetic background. The highly expressed proteins in each cell type were separated and collected in the liquid state where they were analyzed by **matrix-assisted laser desorption/ ionization** time-of-flight **mass spectrometry** (**MALDI**-TOFMS) to obtain the molecular weight of the proteins. The protein fractions were then subjected to tryptic digestion and analyzed by pulsed delay extraction (PDE)-**MALDI**-TOFMS to obtain the **peptide** maps. The expressed proteins were identified based upon the molecular weight and **peptide** map using database-searching procedures. It isshown that key cancer-related proteins can be detected and identified which may be potentially used as biomarkers for cancer detection.
CC Neoplasms and Neoplastic Agents - Biochemistry *24006
Biochemical Methods - General *10050
Biophysics - General Biophysical Studies *10502
Reproductive System - General; Methods *16501
BC Hominidae 86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Tumor Biology
IT Chemicals & Biochemicals
protein: analysis, profiles
IT Methods & Equipment
high performance liquid **chromatography**: liquid **chromatography**, purification method; **matrix-assisted laser desorption/ ionization mass spectrometry**: analytical method, **mass spectrometry**: cb; Beckman System Gold high performance liquid **chromatography** system: Beckman, laboratory equipment; C18 coated silica: packing material
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
MCF-10A cell line (Hominidae): human breast cancer cells; MCF-7 cell line (Hominidae): human breast cancer cells
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

RN 7631-86-9 (SILICA)
7440-57-5 (GOLD)

L92 ANSWER 4 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:304833 BIOSIS
DN PREV199900304833
TI Protein **identification** in SDS PAGE gel bands using mass spectrometry: The need for analysis by complementary methods (**MALDI** vs. nanoflow ESIMS.
AU Medzihradszky, K. F. (1); Leffler, H. (1); Burlingame, A. L. (1)
CS (1) Mass Spectrometry Facility, Department of Pharmaceutical Chemistry, University of California San Francisco, San Francisco, CA, 94143-0446 USA
SO FASEB Journal, (April 23, 1999) Vol. 13, No. 7, pp. A1478.
Meeting Info.: Annual Meeting of the American Societies for Experimental Biology on Biochemistry and Molecular Biology 99 San Francisco, California, USA May 16-20, 1999 American Societies for Experimental Biology
. ISSN: 0892-6638.
DT Conference
LA English
CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Digestive System - General; Methods *14001
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Leporidae 86040
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Parts, Structures, & Systems of Organisms
intestine: digestive system
IT Chemicals & Biochemicals
protein: identification, purification
IT Methods & Equipment
mass spectrometry: spectroscopic techniques: CB; reversed-phase HPLC [reversed-phase high performance liquid **chromatography**]: analytical method; **Matrix-Assisted Laser Desorption Ionization** analysis: analytical method; Nanoflow electrospray analysis: analytical method; QSTAR instrument [quadrupole-time-of-flight instrument]; SDS-PAGE gel bands [SDS-polyacrylamide gel electrophoresis]: purification method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
rabbit (Leporidae)
ORGN Organism Superterms
Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates

L92 ANSWER 5 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:256189 BIOSIS
DN PREV199900256189
TI Protein sequencing by **ISD** and PSD **MALDI-TOF** MS.
AU Suckau, D. (1); Cornett, D. S. (1)
CS (1) Bruker Daltonik GmbH, Fahrenheitstrasse 4, D-28359, Bremen Germany
SO Analusis, (Dec., 1998) Vol. 26, No. 10, pp. M18-M21.
ISSN: 0365-4877.
DT Article
LA English
SL English
AB **Peptide** and protein sequencing techniques are discussed which are available on a **MALDI**-TOF mass spectrometer equipped with an

ion reflector. They allow the fast assignment of at least partial sequences that are sufficient to identify a protein uniquely by library searches and do not require additional enzymatic or **chromatographic** steps.

CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
oxytocin: sequencing; **peptide**: sequencing; protein: sequencing

IT Methods & Equipment
ion-source decay spectra [ISD spectra]: analytical method, optical analysis; **matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** [**MALDI**-TOF MS]: **mass spectrometry**: CB, sequencing method; oxytocin sequencing: sequencing method, sequencing techniques; post-source decay spectra [PSD spectra]: analytical method, optical analysis; REFLEX II **MALDI**-TOF **mass spectrometer**: equipment

RN 50-56-6 (OXYTOCIN)

L92 ANSWER 6 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:247184 BIOSIS
DN PREV199900247184
TI An investigation of residue-specific contributions to **peptide** desorption in **MALDI-TOF** mass spectrometry.
AU Valero, Mari-Luz; Giralt, Ernest; Andreu, David (1)
CS (1) Department of Organic Chemistry, University of Barcelona, E-08028, Barcelona Spain
SO Letters in Peptide Science, (March, 1999) Vol. 6, No. 2-3, pp. 109-115. ISSN: 0929-5666.
DT Article
LA English
SL English
AB The **MALDI**-TOF mass spectra of a set of 240 analogs of the **pentadecapeptide** YTASARGDLAHLTTT, displaying single point replacements with all amino acids except Met, Cys and Trp, have been used to study the contribution of individual residues to **peptide** desorption. Replacements with non-polar aliphatic (except Ala) or aromatic residues at most positions tend to reinforce ion signals relative to the cognate sequence. Among polar residues, Arg shows also a clear tendency to enhance signal intensity at most positions. The responses recorded for replacements with a given amino acid can be averaged and normalized to give a mean response index, Rm, which qualitatively expresses the relative contribution of that residue to the desorption of a generic **peptide**. HPLC analysis of the replacement set does not support a significant role of residue hydrophobicity in **peptide** desorption. The unique role of Arg in promoting **peptide** desorption may be related to a better stabilization of **peptide** -matrix adducts through guanidinium-carboxylate interaction.

CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Comparative Biochemistry, General *10010
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Studies *10502
Biophysics - Molecular Properties and Macromolecules *10506

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
amino acids; **pentadecapeptides**: analysis; **peptide** -matrix adducts: analysis; **peptides**: analysis

IT Methods & Equipment
matrix-assisted laser desorption ionization time-of-flight detection **mass spectrometry**: analytical method, spectroscopic techniques: CB;

Finnigan MAT **Lasermat** 2000 **spectrometer**: Finnigan, equipment; HPLC [high performance liquid **chromatography**]: analytical method, liquid **chromatography**

IT Miscellaneous Descriptors
peptide desorption: analysis, residue-specific

L92 ANSWER 7 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:199570 BIOSIS
DN PREV199900199570
TI A strategy for **rapid** and efficient sequencing of Lys-C **peptides** by **Matrix-assisted laser desorption/ionisation** time-of-flight **mass spectrometry** post-source decay.
AU Pfeifer, Thomas; Ruecknagel, Peter; Kuellertz, Gerhard; Schierhorn, Angelika (1)
CS (1) Department of Biochemistry, University Halle-Wittenberg, Kurt-Mothes-Str. 3, D-06120, Halle/Saale Germany
SO Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 5, pp. 362-369.
ISSN: 0951-4198.
DT Article
LA English
AB A modification procedure for Lys-C **peptides** is described which simplifies the correct assignment of the amino acid sequence. Release of the C-terminal lysine from Lys-C **peptides** by carboxypeptidase B and subsequent N-terminal acetylation of the resulting **peptides** leads to predictable shifts of the C- and N-terminal fragment ions in Matrix-assisted laser desorption/ionisation time-of-flight post-source decay mass spectra and facilitates the correct assignment of mostly complete amino acid sequences for **oligopeptides**. The derived sequences of **peptides** from unknown proteins were used to search in databases for homologous protein sequences. Our method was applied to an unknown protein isolated from eggs of Drosophila melanogaster, resulting in the identification of a peptidyl prolyl cis-trans-isomerase.
CC Biochemical Studies - General *10060
Genetics and Cytogenetics - Animal *03506
Enzymes - General and Comparative Studies; Coenzymes *10802
Invertebrata, Comparative and Experimental Morphology, Physiology and Pathology - Insecta - General *64072
Biochemical Methods - General *10050
BC Diptera 75314
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
carboxypeptidase B; lysine-C **peptides**; **oligopeptides**; peptidyl prolyl cis-trans-isomerase
IT Methods & Equipment
affinity column: laboratory equipment; amino-terminal sequencing: Recombinant DNA Technology, sequencing techniques, gene sequencing method; **matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** post-source decay: analytical method, **mass spectrometry**: CB; reversed-phase high performance liquid **chromatography**: liquid **chromatography**, purification method; sequencing: Recombinant DNA Technology, gene sequencing method, sequencing techniques; Bruker Reflex TOF **mass spectrometer**: Bruker-Franzen, laboratory equipment
ORGN Super Taxa
Diptera: Insecta, Arthropoda, Invertebrata, Animalia
ORGN Organism Name
Drosophila melanogaster (Diptera)
ORGN Organism Superterms
Animals; Arthropods; Insects; Invertebrates
RN 9025-24-5 (CARBOXYPEPTIDASE B)

L92 ANSWER 8 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1999:166959 BIOSIS
DN PREV199900166959
TI **MALDI/peptide** mass **fingerprinting** analysis of complex protein mixtures: Implications for proteomics.
AU Parker, Kenneth C. (1)
CS (1) Perseptive Biosystems, 500 Old Connecticut Path, Framingham, MA 01701 USA
SO Abstracts of Papers American Chemical Society, (1999) Vol. 217, No. 1-2, pp. ANYL 180.
Meeting Info.: 217th National Meeting of the American Chemical Society Anaheim, California, USA March 21-25, 1999 American Chemical Society . ISSN: 0065-7727.
DT Conference
LA English
CC Genetics of Bacteria and Viruses *31500
Genetics and Cytogenetics - General *03502
Biochemical Methods - General *10050
Biochemical Studies - General *10060
BC Enterobacteriaceae 06702
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
protein: analysis, complex mixtures; DNA
IT Methods & Equipment
chromatography: purification method; **peptide** mass fingerprinting: analytical method; **MALDI** [matrix-assisted laser/desorption ionization]: analytical method; SDS gel electrophoresis: analytical method, separation method; 2D gel electrophoresis: analytical method, separation method
IT Miscellaneous Descriptors
proteomics; Meeting Abstract
ORGN Super Taxa
Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
ORGN Organism Name
E. coli [Escherichia coli] (Enterobacteriaceae)
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms

L92 ANSWER 9 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:149127 BIOSIS
DN PREV199900149127
TI **Matrix-assisted laser desorption/ionisation** time-of-flight/thin layer **chromatography/mass spectrometry**: A **rapid** method for impurity testing.
AU Mowthorpe, Siew; Clench, Malcolm R. (1); Cricelius, Anna; Richards, Don S.; Parr, Vic; Tetler, Lee W.
CS (1) Div. Chem., Sch. Sci. Math., Sheffield Hallam Univ., Pond St., Sheffield S1 1WB UK
SO Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 4, pp. 264-270.
ISSN: 0951-4198.
DT Article
LA English
AB Thin layer **chromatography/matrix-assisted laser desorption/ionization mass spectrometry** (TLC/MALD-IMS) has been previously used to obtain **mass** spectra from a variety of compounds, principally **peptides**. For pharmaceutical compounds, which are often of relatively low molecular weight, it is important that any **matrix** materials employed do not interfere with the **mass** spectra obtained. The key step to successful TLC/**MALDI**-MS is hence the preparation of the TLC plate prior to **mass spectrometry** . Crucial to this is the deposition of **matrix** material into the

plate to promote co-crystallization with the analyte. In this work we have examined the literature methods for plate preparation and developed two new approaches. The first involves brushing the TLC plate with a supersaturated solution of **matrix** and the second involves electrospraying the TLC plate with a **matrix** solution. Data are presented from the direct analysis of tetracycline and its impurities. Using the electrospray method the limit of detection for tetracycline is 1 ng from a TLC plate. A commercial **MALDI**-TOF **mass spectrometer** has been modified to allow the acquisition of **chromatographic** data from TLC plates. **Chromatograms** from replicate spots of 100 and 1 mug of tetracycline are shown.

CC Pharmacology - General *22002
Biochemical Methods - General *10050
Biophysics - General Biophysical Studies *10502
Chemotherapy - General; Methods; Metabolism *38502

IT Major Concepts
Methods and Techniques; Pharmacology

IT Chemicals & Biochemicals
anhydrotetracycline: Pfizer Central Research, pharmaceutical impurity, tetracycline manufacturing impurity, analysis; compound iv: Pfizer Central Research, pharmaceutical impurity, tetracycline manufacturing impurity, analysis; epitetracycline: Pfizer Central Research, pharmaceutical impurity, tetracycline manufacturing impurity, analysis; tetracycline: Sigma-Aldrich, analysis, pharmaceutical

IT Methods & Equipment
matrix-assisted laser desorption /ionisation time-of-flight/thin layer **chromatography /mass spectrometry**: analytical method, **chromatographic** techniques: cb, **mass spectrometry**: cb, purification method; **LaserTOF** 1500 **mass spectrometer**: Scientific Analytical Instruments, modified, laboratory equipment

IT Miscellaneous Descriptors
rapid pharmaceutical impurities testing

RN 60-54-8 (TETRACYCLINE)
79-85-6 (EPITETRACYCLINE)
1665-56-1 (ANHYDROTETRACYCLINE)

L92 ANSWER 10 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:90964 BIOSIS
DN PREV199900090964
TI Liquid **chromatography**/microspray mass spectrometry for **bacterial** investigations.
AU Krishnamurthy, Thaiya (1); Davis, Michael T.; Stahl, Douglas C.; Lee, Terry D.
CS (1) R and T Directorate, US Army Edgewood RD and E Center, Aberdeen Proving Groun, MD 21010-5423 USA
SO Rapid Communications in Mass Spectrometry, (1999) Vol. 13, No. 1, pp. 39-49.
ISSN: 0951-4198.
DT Article
LA English
AB Cellular proteins (biomarkers) specific to any individual microorganism, determined by the direct **mass** spectral analysis of the corresponding intact cellular suspension, can be applied for the rapid and specific identification of the organisms present in unknown samples. The components of the bacterial suspensions, after a rapid separation over a C18 reversed-phase microcapillary column, were directly subjected to on-line electrospray **ionization** followed by analysis using an ion trap tandem **mass spectrometer**. This approach is equally effective for gram-positive as well as gram-negative bacteria but has a distinct advantage over our earlier reported method involving **matrix-assisted laser desorption/ ionization** time-of-flight **mass spectrometry** (**MALDI**-TOFMS). During electrospray **ionization mass spectrometry** (ESI-MS), liquid samples can be

directly analyzed and there is the potential for developing tandem **mass** spectral methods for more specific identification of the individual organisms present in crude bacterial mixtures. The total analysis time leading to unambiguous bacterial identification in samples was less than 10 minutes and the results were quite reproducible. Miniaturization of the instrumentation along with total automation of this simple process could have immense impact on field operations. Routine, rapid, cost-effective field monitoring of environmental samples, agricultural products, samples from food processing, industrial sites and health institutions for suspected bacterial contamination could be a reality in the near future. Potential utility in biological, medical, bioprocessing, pharmaceutical, and other industrial research is also enormous.

CC **Biophysics - General Biophysical Techniques *10504**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Physiology and Biochemistry of Bacteria *31000
Medical and Clinical Microbiology - Bacteriology *36002

BC Gram-Negative Aerobic Rods and Cocci 06500
Enterobacteriaceae 06702
Endospore-forming Gram-Positives 07810

IT Major Concepts
Infection; Methods and Techniques

IT Chemicals & Biochemicals
cellular proteins: analysis, bacterial biomarkers, separation

IT Methods & Equipment
electrospray **ionization mass spectrometry**
: analytical method, **mass spectrometry**: CB;
matrix-assisted laser desorption/
ionization time-of-flight **mass spectrometry**
: analytical method, **mass spectrometry**: CB; C-18
reversed-phase microcapillary column: equipment; HPLC [high performance liquid **chromatography**]: analytical method, liquid **chromatography**

ORGN Super Taxa
Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Gram-Negative Aerobic Rods and Cocci: Eubacteria, Bacteria, Microorganisms

ORGN Organism Name
Bacillus cereus (Endospore-forming Gram-Positives); Bacillus subtilis (Endospore-forming Gram-Positives); Bacillus thuringiensis (Endospore-forming Gram-Positives); Brucella melitensis (Gram-Negative Aerobic Rods and Cocci); Francisella tularensis (Gram-Negative Aerobic Rods and Cocci); Yersinia pestis (Enterobacteriaceae)

ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms

L92 ANSWER 11 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:63823 BIOSIS
DN PREV199900063823
TI A **rapid** and sensitive procedure for the micro-purification and subsdequent characterization of **peptides** and protein samples by N-terminal sequencing and **matrix assisted laser desorption ionization** time of flight **mass spectrometry**.
AU Grimm, R.; Grasser, K. D.; Kubach, J.; Hancock, W. S. (1)
CS (1) Hewlett-Packard, Chem. Analysis Group Europe, 76337 Waldbronn Germany
SO Journal of Pharmaceutical and Biomedical Analysis, (Dec., 1998) Vol. 18, No. 4-5, pp. 545-554.
ISSN: 0731-7085.
DT Article
LA English
AB The characterization of the proteome, a key activity in the post-genome era, is made extremely challenging by the microheterogeneity introduced by post translational modifications such as glycosylation in the diverse set of proteins expressed in a cellular system. High resolution separation

systems, such as 2D-gel electrophoresis and more recently liquid **chromatography** (LC) have been used to fractionate these complex mixtures, however, subsequent **mass** analysis is hindered by the low level of the purified components. Off-line coupling of **matrix assisted laser desorption ionization** time of flight **mass spectrometry** (**MALDI**-TOF/MS) is an attractive technique for the analysis of such samples, but suffers from sensitivity to the degree of salt contamination that is unavoidable in the isolation of low level protein samples from biological extracts. In this publication we will report on a novel application of a commercially available system for the micro-purification of **peptides** and proteins. In this procedure micro-columns (normally used for sequencing of electroblotted samples) were used to rapidly purify protein digests or crude extracts of proteins in sufficient amounts for further analyses by protein sequencing and **MALDI**-TOF/MS. To demonstrate the applicability of the these techniques we isolated and performed structural analysis of the following samples: a high-mannose **glycopeptide** isolated from a digest of the glycoprotein rt-PA, a poly-His tagged recombinant DNA-binding protein isolated by Ni2+-chelating agarose and a polyclonal antibody sample.

CC Pharmacology - General *22002
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504

IT Major Concepts
Methods and Techniques; Pharmacology

IT Chemicals & Biochemicals
high-mannose glycoprotein: characterization, purification; **peptides**: characterization, purification; poly-histidine tagged recombinant DNA-binding protein: characterization, purification; protein samples: characterization, purification

IT Methods & Equipment
column purification: Isolation/Purification Techniques: CB, purification method; **matrix assisted laser desorption ionization** time of flight **mass spectrometry**: analytical method, **mass spectrometry**: CB; reversed-phase HPLC [reversed phase high performance liquid **chromatography**]: analytical method, high performance liquid **chromatography**; HP G2025A instrument: equipment; HP 1090 Series II HPLC system: equipment; N-terminal protein sequencing: protein sequencing, sequencing method

RN 26062-48-6Q (POLY-HISTIDINE)
26854-81-9Q (POLY-HISTIDINE)

L92 ANSWER 12 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:63376 BIOSIS
DN PREV199900063376
TI **Rapid identification** and screening of proteins from whole cell lysates of human erythroleukemia cells in the liquid phase, using non-porous reversed phase high-performance liquid **chromatography** separations of proteins followed by multi-assisted laser desorption/ionization mass spectrometry analysis and sequence **database** searching.
AU Chen, Yajuan; Wall, Dan; Lubman, David M. (1)
CS (1) Dep. Chemistry, University Michigan, 930 N. University Ave., Ann Arbor, MI 48109-1055 USA
SO Rapid Communications in Mass Spectrometry, (1998) Vol. 12, No. 24, pp. 1994-2003.
ISSN: 0951-4198.
DT Article
LA English
AB Non-porous reversed phase (NPRP) high-performance liquid **chromatography** (HPLC) has been used as a rapid method to separate proteins from whole cell lysates of human erythroleukemia (HEL) cells. Using phosphate-buffered saline (PBS) as a lysis buffer to extract proteins from HEL cells, more than 100 proteins of molecular weight up to 30 kDa were separated by the NPRP HPLC method, using a programmed

acetonitrile:H2O gradient. The separated proteins were collected as liquid fractions as they eluted, and were further separated on the NPRP column with a different gradient to separate coeluting peaks. The isolated protein fractions were analyzed by **matrix-assisted laser desorption/ionization mass spectrometry** (**MALDI**-MS) to determine the molecular weight of the protein. The proteins were cleaved by chemical or enzymatic digestion to produce **peptide** maps, which were analyzed by pulsed delayed extraction **MALDI**-MS. The **peptide** maps were matched against a database search to determine the protein identity. In some cases, several enzymes were used in order to find exactly one match against the database. This methodology is demonstrated for several proteins isolated from HEL cells and identified via database matching.

CC Neoplasms and Neoplastic Agents - General *24002
Cytology and Cytochemistry - Human *02508
Biochemical Methods - General *10050
Biophysics - General Biophysical Studies *10502
Blood, Blood-Forming Organs and Body Fluids - General; Methods *15001

BC Hominidae 86215

IT Major Concepts
Methods and Techniques; Tumor Biology

IT Parts, Structures, & Systems of Organisms
erythroleukemia cells: blood and lymphatics, immune system, whole cell lysates

IT Diseases
erythroleukemia: blood and lymphatic disease, neoplastic disease

IT Chemicals & Biochemicals
phosphate-buffered saline: lysis buffer; protein: analysis, rapid identification, screening

IT Alternate Indexing
Leukemia, Erythroblastic, Acute (MeSH)

IT Methods & Equipment
multi-assisted laser desorption/ionization mass spectrometry: analytical method, mass spectrometry: cb; non-porous reversed phase high performance liquid **chromatography**: high performance liquid **chromatography**, purification method; sequence database searching: Analysis/Characterization Techniques: cb, analytical method; Beckman System Gold high performance liquid **chromatograph**: Beckman, laboratory equipment

IT Miscellaneous Descriptors
proteomics

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae)

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

RN 14265-44-2 (PHOSPHATE)
7440-57-5 (GOLD)

L92 ANSWER 13 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1999:23890 BIOSIS
DN PREV199900023890
TI **Identification** of proteins by **matrix-assisted laser desorption/ionization mass spectrometry** using **peptide** and fragment ion **masses.**
AU Courchesne, Paul L.; Patterson, Scott D.
CS Protein Structure, Amgen Inc., Thousand Oaks, CA USA
SO Link, A. J.. Methods in Molecular Biology, (1999) Vol. 112, pp. 487-511. Methods in Molecular Biology; 2-D proteome analysis protocols. Publisher: Humana Press Inc. Suite 808, 999 Riverview Drive, Totowa, New Jersey 07512, USA.
ISSN: 0097-0816. ISBN: 0-89603-524-7.
DT Book
LA English

CC **Biochemical Methods - General *10050**
Biochemical Studies - General *10060
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
protein: identification
IT Methods & Equipment
enzymatic digestion in-gel: characterization method, chemical modification, protocol; enzymatic digestion on Immobilon-CD: characterization method, protocol, chemical modification; enzymatic digestion on Immobilon-P: characterization method, protocol, chemical modification; **matrix-assisted laser/ desorption ionization/ionization mass spectrometry**: Analysis/Characterization
Techniques: CB, analytical method; microcolumn **chromatography** : **chromatographic** techniques, protocol, purification method; two-dimensional gel electrophoresis: polyacrylamide gel electrophoresis, separation method
IT Miscellaneous Descriptors
Book Chapter
RN 9003-05-8 (POLYACRYLAMIDE)

L92 ANSWER 14 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:473370 BIOSIS
DN PREV199800473370
TI **Coupling** capillary high-performance liquid **chromatography** to **matrix-assisted laser desorption/ionization mass spectrometry** and N-terminal sequencing of **peptides** via automated microblotting onto membrane substrates.
AU Stevenson, Tracy I.; Loo, Joseph A.; Greis, Kenneth D. (1)
CS (1) Procter and Gamble Pharmaceuticals, P.O. Box 8006, Mason, OH 45040 USA
SO Analytical Biochemistry, (Sept. 10, 1998) Vol. 262, No. 2, pp. 99-109. ISSN: 0003-2697.
DT Article
LA English
AB To minimize low-quantity sample handling for protein sequencing and **matrix-assisted laser desorption/ ionization** (**MALDI**) **mass spectrometry** , a system consisting of an HPLC interfaced to an automated blotting device was used for off-line sample collection. Typically, protein digests are separated by reverse-phase HPLC and the resulting **peptide** fractions are pooled, concentrated, and then subjected to N-terminal sequence analysis. Obtaining unambiguous sequence from **peptides** derived from protein digestion at subpicomole levels requires careful sample handling to prevent loss of sample. In cases where multiple sequences are present, a secondary method such as **mass spectrometry** is needed to confirm the identity of the **peptides**. To minimize sample handling, commercial microblotting instruments have become available to deposit **peptides** directly onto polyvinylidene difluoride (PVDF) membrane for automated N-terminal sequence analysis. In order to adapt this technology to **mass spectrometry**, we investigated the use of **MALDI**-MS compatible membranes such as Teflon and polyethylene (PE) as the blotting media for fraction collection. Using a panel of standard **peptides** as well as protein digests, we demonstrate that **peptides** separated by capillary HPLC can be collected directly onto Teflon or PE and detected into the femtomole range. Furthermore, detailed sequence analysis could be obtained by postsource decay fragmentation spectra of individual **peptides** blotted onto either PE or Teflon. Due to the high sensitivity of the **MALDI**-MS from these membranes, it was discovered that the small amount of **peptide** that passed through the PVDF membrane during a collection of **peptides** for N-terminal sequencing was sufficient to be collected and **mass** analyzed from a second underlying **MALDI**-MS compatible membrane. Therefore, from a single HPLC separation, samples could be collected onto

both PVDF for traditional N-terminal sequencing and PE or Teflon for **MALDI**-MS. We demonstrate the general utility of this method for sequencing **peptides** from a tryptic digestion at subpicomole levels and for identifying unknown proteins separated by 2-dimensional gel electrophoresis. The ability to generate both N-terminal sequence and confirmatory **mass** information from multiple **peptides** in a single separation greatly improves the reliability and the accuracy of protein characterization at subpicomole levels.

CC Biochemical Studies - General *10060
Biochemical Methods - General *10050

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
peptides

IT Methods & Equipment
automated microblotting: Recombinant DNA Technology, gene sequencing method, sequencing techniques; capillary high performance liquid **chromatography**: liquid **chromatography**, separation method; **matrix-assisted laser desorption/ionization mass spectrometry**: analytical method, **mass spectrometry**: CB; polyethylene membranes: laboratory equipment; polyvinylidene difluoride membrane: laboratory equipment; sequence analysis: Analysis/Characterization Techniques: CB, analytical method; Applied Biosystems Procise Model 492 protein sequencer: Applied Biosystems, laboratory equipment; ABI Model 785A programmable absorbance detector: ABI, laboratory equipment; Brownlee C-18 column: laboratory equipment; N-terminal sequencing: Recombinant DNA Technology, gene sequencing method, sequencing techniques; Perkin-Elmer/ABI Model 140D microgradient delivery system: ABI, laboratory equipment, Perkin-Elmer; PerSeptive Biosystems, Inc. Voyager Elite-DE time-of-flight **mass spectrometer**: PerSeptive Biosystems, Inc., laboratory equipment; SDS-polyacrylamide gel electrophoresis: polyacrylamide gel electrophoresis, separation method; Teflon membranes: Millipore Corp., laboratory equipment; 2-dimensional gel electrophoresis: electrophoretic techniques, separation method

IT Miscellaneous Descriptors
membrane substrates; protein digestion; sample handling

RN 24937-79-9 (POLYVINYLIDENE DIFLUORIDE)
9002-84-0 (TEFLON)
9002-88-4 (POLYETHYLENE)

L92 ANSWER 15 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:407472 BIOSIS
DN PREV199800407472
TI **Matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** analysis of proteins in human **cerebrospinal** fluid.
AU Westman, A. (1); Nilsson, C. L.; Ekman, R.
CS (1) Inst. Clinical Neurosci., Dep. Psychiatry Neurochemistry, Goteborg Univ., Sahlgrenska Univ. Hospital/Molndal, S-431 80 Molndal Sweden
SO Rapid Communications in Mass Spectrometry, (1998) Vol. 12, No. 16, pp. 1092-1098.
ISSN: 0951-4198.
DT Article
LA English
AB **Matrix-assisted laser desorption/ionization** time-of-flight **mass** spectra of proteins in cerebrospinal fluid analyzed without prior purification are presented. Less than 100 fmol amounts of proteins in the 10000 to 20000 u **mass** range and linked to human disease (multiple sclerosis, Alzheimer's disease, and stroke) were detected in a complex mixture of proteins and **peptides**, in the presence of high concentrations of salts, lipids and free amino acids. The **mass** resolution was sufficient to distinguish between the non-hydroxylated and hydroxylated

forms of a 13 400 u protein. Simple fractionation of the cerebrospinal fluid using microbore-reversed phase high performance liquid **chromatography** improved signal-to-noise ratios in the **mass** spectra. High-accuracy **peptide mass** mapping and database searching were utilized to confirm the identity of several proteins. The presented results show that **matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** could be used as a tool to perform rapid screening of chemically altered proteins in small volumes of biological fluids.

CC Nervous System - General; Methods *20501
Biochemical Methods - General *10050
Biochemical Studies - General *10060

BC Hominidae 86215

IT Major Concepts
Methods and Techniques; Nervous System (Neural Coordination)

IT Parts, Structures, & Systems of Organisms
cerebrospinal fluid: nervous system

IT Diseases
multiple sclerosis: immune system disease, nervous system disease; stroke: nervous system disease, vascular disease; Alzheimer's disease: behavioral and mental disorders, nervous system disease

IT Chemicals & Biochemicals
proteins

IT Methods & Equipment
high-accuracy **peptide mass** mapping: Analysis/Characterization Techniques: CB, analytical method; **matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** : analytical method, spectroscopic techniques: CB; microbore-reversed phase high performance liquid **chromatography**: fractionation method, liquid **chromatography**; mu-RPC C2/C18 column: Pharmacia, laboratory equipment; seed layer method: preparation method, specimen preparation techniques; Reflex **MALDI**-TOF **mass spectrometer**: Bruker-Franzen Analytik GmbH, laboratory equipment; SMART system: Pharmacia LKB Biotechnology Uppsala, laboratory equipment; Western blot: analytical method, gene mapping, detection/labeling techniques

IT Miscellaneous Descriptors
database searching; mass resolution

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae): patient

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L92 ANSWER 16 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:297352 BIOSIS
DN PREV199800297352
TI Routine **identification** of proteins from sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels or polyvinyl difluoride membranes using **matrix assisted laser desorption/ionization**-time of flight-**mass spectrometry** (**MALDI-TOF**-MS.
AU Fernandez, Joseph; Gharahdaghi, Farzin; Mische, Sheenah M. (1)
CS (1) Rockefeller Univ., P.O. Box 105, 1230 York Ave., New York, NY 10021 USA
SO Electrophoresis, (May, 1998) Vol. 19, No. 6, pp. 1036-1045. ISSN: 0173-0835.
DT Article
LA English
AB As the resource laboratory for Rockefeller University our emphasis continues to be on methodology development for the routine analysis of low abundance proteins isolated from native sources. In the past ten years, gel electrophoresis of proteins has become the method of choice for the

preparation of microgram and submicrogram quantities of protein for primary structural characterization, and over 95% of the samples submitted for protein identification are either in a gel or bound to polyvinyl difluoride membranes (PVDF). As such, we employ multiple microanalytical approaches encompassing Edman sequence degradation, amino acid and **matrix assisted laser desorption/ ionization**-time of flight (**MALDI**-TOF) **mass spectrometric** analysis to provide an integrated protein characterization of such samples. Here we describe the two major services we employ when providing protein identification from in-gel or PVDF-bound proteins.

CC **Biophysics - General Biophysical Techniques *10504**
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
protein: analysis

IT Methods & Equipment
matrix assisted laser desorption /ionization-time of flight-**mass spectrometry**: analytical method, spectroscopic techniques; Applied Biosystems 470 instrument: equipment; Edman sequence degradation: sequencing method, sequencing techniques; Hewlett-Packard G1000A instrument: equipment; Perkin Elmer/Applied Biosystem 494 Procise instrument: equipment; SDS-polyacrylamide gel electrophoresis: analysis/characterization techniques, analytical method, electrophoretic techniques; 492 Procise cLc high performance liquid **chromatography** system: Perkin Elmer/Applied Biosystems, equipment

IT Miscellaneous Descriptors
polyvinyl difluoride membranes

RN 7440-23-5 (SODIUM)

L92 ANSWER 17 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:297345 BIOSIS
DN PREV199800297345
TI **Rapid identification** of comigrating gel-isolated proteins by ion trap-mass spectrometry.
AU Arnott, David; Henzel, William J.; Stults, John T. (1)
CS (1) Genentech Inc., 1 DNA Way, South San Francisco, CA 94080 USA
SO Electrophoresis, (May, 1998) Vol. 19, No. 6, pp. 968-980.
ISSN: 0173-0835.
DT Article
LA English
AB In the search for novel nuclear binding proteins, two bands from a sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gel were analyzed and each was found to contain a number of proteins that subsequently were identified by tandem **mass spectrometry** (MS/MS) on a quadrupole ion trap instrument. The bands were digested with trypsin in situ on a polyvinylidene difluoride (PVDF) membrane following electroblot transfer. Analysis of a 2.5% aliquot of each **peptide** mixture by **matrix assisted laser desorption/ionization-mass spectrometry** (**MALDI**-MS) followed by an initial database search with the **peptide masses** failed to identify the proteins. The **peptides** were separated by reversed-phase capillary high performance liquid **chromatography** (HPLC) in anticipation of subsequent Edman degradation, but **mass** analysis of the **chromatographic** fractions by **MALDI**-MS revealed multiple, coeluting **peptides** that precluded this approach. Selected fractions were analyzed by capillary HPLC-electrospray **ionization**-ion trap **mass spectrometry**. Tandem **mass spectrometry** provided significant fragmentation from which full or partial sequence was deduced for a number of **peptides**. Two stages of fragmentation (MS) were used in one case

to determine additional sequence. Database searches, each using a single **peptide mass** plus partial sequence, identified four proteins from a single electrophoretic band at 45 kDa, and four proteins from a second band at 60 kDa. Many of these proteins were derived from human keratin, The protein identifications were corroborated by the presence of multiple matching **peptide masses** in the **MALDI**-MS spectra. In addition, a novel sequence, not found in protein or DNA databases, was determined by interpretation of the MS/MS data. These results demonstrate the power of the quadrupole ion trap for the identification of multiple proteins in a mixture, and for de novo determination of **peptide** sequence. Reanalysis of the fragmentation data with a modified database searching algorithm showed that the same sets of proteins were identified from a limited number of fragment ion **masses**, in the absence of **mass** spectral interpretation or amino acid sequence. The implications for protein identification solely from fragment ion **masses** are discussed, including advantages for low signal levels, for a reduction of the necessary interpretation expertise, and for increased speed.

CC **Biophysics - General Biophysical Techniques *10504**
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
comigrating gel-isolated proteins: analysis

IT Methods & Equipment
high performance liquid **chromatography** system: Waters Associates, equipment; ion trap-**mass spectrometry**: analytical method, spectroscopic techniques; **matrix assisted laser desorption-ionization mass spectrometry**: analytical method, spectroscopic techniques; protein analysis: analytical method, methodological approach; HPLC [high performance liquid **chromatography**]: analysis/characterization techniques, analytical method, **chromatographic** techniques; SDS-polyacrylamide gel electrophoresis: analytical method, electrophoretic techniques

L92 ANSWER 18 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:297017 BIOSIS
DN PREV199800297017
TI **Peptide mass fingerprint** sequence coverage from differently stained proteins on two-dimensional electrophoresis patterns by **matrix assisted laser desorption/ionization-mass spectrometry** (**MALDI**-MS.
AU Scheler, Christian; Lamer, Stephanie; Pan, Zaoming; Li, Xin-Ping; Salnikow, Johannes; Jungblut, Peter (1)
CS (1) Max-Planck-Inst. Infectionbiol., Proteinanalysis, Monbijoustr. 2, D-10117 Berlin Germany
SO Electrophoresis, (May, 1998) Vol. 19, No. 6, pp. 918-927. ISSN: 0173-0835.
DT Article
LA English
AB Identification of proteins separated by two-dimensional electrophoresis (2-DE) is a necessary task to overcome the purely descriptive character of 2-DE and a prerequisite to the construction of 2-DE databases in proteome projects. **Matrix assisted laser desorption/ionization-mass spectrometry** (**MALDI**-MS) has a sensitivity for **peptide** detection in the lower fmol range, which should be sufficient for an analysis of even weakly silver-stained protein spots by **peptide mass** fingerprinting. Unfortunately, proteins are modified by the silver staining procedure, leading to low sequence coverage. Omission of glutaraldehyde increased the sequence coverage, but this improved sequence coverage is still clearly below the sequence

coverage starting with Coomassie Brilliant Blue (CBB) R-250-stained spots. Other factors additionally seem to modify proteins during silver staining. By decreasing the protein amount, the advantage of very sensitive detection on the gel is lost during identification, because the resulting low sequence coverage is not sufficient for secure identification. Low-quantity proteins can be identified better starting with CBB G-250 or Zn-imidazol-stained proteins. In contrast, for high-quantity CBB R-250-stained spots, a sequence coverage of up to 90% can be obtained by using only one cleaving enzyme, and up to 80% was reached for medium-quantity spots after combination of tryptic digest with Asp-N- and Glu-C digest.

CC **Biochemical Studies - Proteins, Peptides and Amino Acids *10064**
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biophysics - General Biophysical Techniques *10504

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
protein: analysis

IT Methods & Equipment
matrix assisted laser desorption /ionization-mass spectrometry: analytical method, spectroscopic techniques; **peptide mass** fingerprint sequencing: sequencing method, sequencing techniques; silver staining: detection/labeling techniques, labeling method; time-of-flight-**matrix assisted laser desorption/ionization mass spectrometer**: equipment; two-dimensional electrophoresis: analytical method, electrophoretic techniques; HPLC [high performance liquid **chromatography**]: analysis/characterization techniques, analytical method, **chromatographic** techniques

RN 7440-22-4 (SILVER)

L92 ANSWER 19 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:266609 BIOSIS
DN PREV199800266609
TI Comprehensive two-dimensional high-performance liquid **chromatography** for the isolation of overexpressed proteins and proteome **mapping**.
AU Opiteck, Gregory J.; Ramirez, Suzanne M.; Jorgenson, James W. (1); Moseley, M. Arthur, III
CS (1) Dep. Chem., Univ. North Carolina Chapel Hill, Venable Hall, CB 3290, Chapel Hill, NC 27599-3290 USA
SO Analytical Biochemistry, (May 1, 1998) Vol. 258, No. 2, pp. 349-361. ISSN: 0003-2697.
DT Article
LA English
AB A two-dimensional liquid **chromatographic** system is described here which uses size-exclusion liquid **chromatography** (SEC) followed by reversed-phase liquid **chromatography** (RPLC) to separate the mixture of proteins resulting from the lysis of Escherichia coli cells and to isolate the proteins that they produce. The size-exclusion **chromatography** can be conducted under either denaturing or nondenaturing conditions. Peaks eluting from the first dimension are automatically subjected to reversed-phase **chromatography** to separate similarly sized proteins on the basis of their various hydrophobicities. The RPLC also serves to desalt the analytes so that they can be detected in the deep ultraviolet region at 215 nm regardless of the SEC mobile phase used. The two-dimensional (2D) **chromatograms** produced in this manner then strongly resemble the format of stained 2D gels, in that spots are displayed on a X-Y axis and intensity represents quantity of analyte. Following **chromatographic** separation, the analytes are deposited into six 96-well (576 total) polypropylene microtiter plates via a fraction collector. Interesting fractions are analyzed by **matrix-assisted laser desorption ionization** time-of-flight **mass spectrometry** (**MALDI**

-TOF/MS) or electrospray **mass spectrometry** (ESI/MS) depending on sample concentration, which both yield accurate (2 to 0.02%) molecular weight information on intact proteins without any additional sample preparation, electroblotting, destaining, etc. The remaining 97% of a fraction can then be used for other analyses, such Edman sequencing, amino acid analysis, or proteolytic digestion and sequencing by tandem **mass spectrometry**. This 2D HPLC protein purification and identification system was used to isolate the src homology (SH2) domain of the nonreceptor tyrosine kinase pp60c-src and beta-lactamase, both inserted into E. coli, as well as a number of native proteins comprising a small portion of the E. coli proteome.

CC **Biochemical Studies - Proteins, Peptides and Amino Acids *10064**
Biophysics - General Biophysical Techniques *10504
Physiology and Biochemistry of Bacteria *31000

BC Enterobacteriaceae 06702

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
proteins: isolation

IT Methods & Equipment
electrospray **mass spectrometry**: analytical method, spectroscopic techniques; **matrix-assisted laser desorption ionization** time-of-flight **mass spectrometry**: analytical method, spectroscopic techniques; reversed-phase liquid **chromatography** UV detection: **chromatography**, separation method; size-exclusion **chromatography**: **chromatographic** techniques, separation method; two-dimensional high-performance liquid **chromatography**: **chromatography**, separation method; API100 single quadrupole **mass spectrometer**: equipment; Edman sequencing: sequencing method, sequencing techniques

IT Miscellaneous Descriptors
proteome mapping

ORGN Super Taxa
Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms

ORGN Organism Name
Escherichia-coli (Enterobacteriaceae)

ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms

L92 ANSWER 20 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS

AN 1998:130807 BIOSIS

DN PREV199800130807

TI **Development** of liquid **chromatography-mass spectrometry** using continuous-flow **matrix-assisted laser desorption ionization** time-of-flight **mass spectrometry**.

AU Whittal, Randy M.; Russon, Larry M.; Li, Liang (1)

CS (1) Dep. Chem., Univ. Alberta, Edmonton, AB T6G 2G2 Canada

SO Journal of Chromatography A, (Jan. 23, 1998) Vol. 794, No. 1-2, pp. 367-375.
ISSN: 0021-9673.

DT Article

LA English

AB The general approach of combining liquid **chromatography** (LC) with **matrix-assisted laser desorption ionization** (**MALDI**) **mass spectrometry** for on-tine detection of **peptides** and proteins based on the use of a continuous-flow (cf) probe is presented. Recent advances in time-of-flight **mass spectrometric** instrumentation for cf-**MALDI** are reported. Using 3-nitrobenzyl alcohol (3-NBA) as the liquid **matrix**, stable flow can be readily achieved and the three-port inter-face does not introduce **chromatographic** peak shape degradation for LC-MS. Separation and detection of low picomoles of **peptides** and proteins can be done

with cf-**MALDI**-LC-MS. Parallel ion extraction and time-lag focusing are shown to provide enhanced performance with regard to **mass** resolution. However, **mass** resolution is generally poor for proteins with **masses** above apprx 6000 u. Strong adduct ion formation with the use of 3-NBA as the liquid **matrix** is believed to be the main cause of this resolution reduction. It is argued that cf-**MALDI** is a technically viable approach for LC-MS, but the overall performance and wide use of this method depend on the discovery of new liquid **matrices** that are suitable for continuous flow and provide much enhanced utility for **MALDI** over 3-NBA, particularly for proteins.

CC **Biophysics - General Biophysical Techniques *10504**
Biochemical Studies - Proteins, Peptides and Amino Acids *10064

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
peptides; proteins

IT Methods & Equipment
continuous-flow **matrix-assisted laser desorption ionization** time-of-flight **mass spectrometry**: analytical method; liquid **chromatography -mass spectrometry**: analytical method, development

L92 ANSWER 21 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:14113 BIOSIS
DN PREV199800014113
TI **Laser desorption mass spectrometry**
.
AU Moore, William T. (1)
CS (1) Protein Chem. Lab., Dep. Pathol. Lab. Med., Sch. Med., Univ. Pennsylvania, Philadelphia, PA 19104 USA
SO Fields, G. B. [Editor]. Methods in Enzymology, (1997) Vol. 289, pp. 520-542. Methods in Enzymology; Solid-phase peptide synthesis. Publisher: Academic Press, Inc. 1250 Sixth Ave., San Diego, California 92101, USA.
ISSN: 0076-6879. ISBN: 0-12-182190-0.
DT Book
LA English
CC **Biochemical Methods - General *10050**
Biochemical Studies - General *10060

IT Major Concepts
Methods and Techniques

IT Methods & Equipment
automated **peptide** synthesis: synthetic method; enzymatic treatment: analytical method; high performance liquid **chromatography**: analytical method; **matrix-assisted laser desorption-ionization mass spectrometry**: analytical method

IT Miscellaneous Descriptors
disulfide bond formation; sample preparation; synthetic **peptide** racemization; Book Chapter

RN 16734-12-6 (DISULFIDE)

L92 ANSWER 22 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1997:407482 BIOSIS
DN PREV199799713685
TI Identification of proteins by **matrix-assisted laser desorption ionization-mass spectrometry** following in-**gel** digestion in low-salt, nonvolatile buffer and simplified **peptide** recovery.
AU Fountoulakis, Michael; Langen, Hanno (1)
CS (1) F. Hoffmann-La Roche Ltd., Pharm. Res. Gene Technol., Basel Switzerland
SO Analytical Biochemistry, (1997) Vol. 250, No. 2, pp. 153-156.
ISSN: 0003-2697.

DT Article
LA English
AB **Matrix-assisted laser desorption ionization-mass spectrometry** is an efficient analytical method for large-scale identification of proteins separated by two-dimensional polyacrylamide gel electrophoresis. Following in-gel digestion, the salt present in the **peptide** extracts is usually removed by **chromatography** prior to analysis. Desalting is a labor-intensive and time-consuming step, limiting the total number of samples that can be processed daily. We improved the daily sample output by performing the in-gel protein digestion in low-salt, nonvolatile buffer and simplifying the recovery of the generated **peptides**, collecting them in a small volume by sonication. This technique is routinely used for identification of proteins of Haemophilus influenzae and human brain. The methodology described facilitates the analytical process and allows the analysis of hundreds of proteins per day. Furthermore, it represents an essential step toward process automation.
CC Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Studies *10502
Physiology and Biochemistry of Bacteria *31000
BC Pasteurellaceae 06703
Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Physiology; Radiology (Medical Sciences)
IT Chemicals & Biochemicals
POLYACRYLAMIDE
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND BIOPHYSICS; BRAIN; DIGESTION METHOD; IN-GEL DIGESTION; LARGE SCALE PROTEIN IDENTIFICATION; **MATRIX-ASSISTED LASER DESORPTION IONIZATION-MASS SPECTROMETRY**; METHODOLOGY; NERVOUS SYSTEM; NONVOLATILE LOW-SALT BUFFER; POLYACRYLAMIDE GEL ELECTROPHORESIS; SEPARATION METHOD; SIMPLIFIED **PEPTIDE** RECOVERY
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Pasteurellaceae: Eubacteria, Bacteria
ORGN Organism Name
human (Hominidae); Haemophilus influenzae (Pasteurellaceae)
ORGN Organism Superterms
animals; bacteria; chordates; eubacteria; humans; mammals; microorganisms; primates; vertebrates
RN 9003-05-8 (POLYACRYLAMIDE)

L92 ANSWER 23 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1997:385385 BIOSIS
DN PREV199799684588
TI High-sensitivity **peptide mapping** by micro-LC with on-line membrane blotting and subsequent **detection** by scanning-IR-**MALDI** mass spectrometry.
AU Eckerskorn, Christoph (1); Strupat, Kerstin; Kellermann, Josef; Lottspeich, Friedrich; Hillenkamp, Franz
CS (1) Max-Planck-Inst. Biochem., 82152 Martinsried Germany
SO Journal of Protein Chemistry, (1997) Vol. 16, No. 5, pp. 349-362. ISSN: 0277-8033.
DT Article
LA English
AB A novel approach to the on-line **mass** determination of **peptides** from digested proteins by scanning infrared **matrix-assisted laser desorption/ ionization** (scanning-IR-**MALDI**) is described. The **peptides** were continuously collected directly onto a PVDF (polyvinylidene fluoride) strip during a HPLC run. Individual

peptides were detected by lining up the PVDF strip with the UV trace from the HPLC run, using visible dye markers as reference points. The local resolution of the **peptides** on the PVDF membrane is preserved during **matrix** incubation for **MALDI**-MS as shown by comparing the UV **chromatogram** and the total ion current (TIC) from an on-line coupled electrospray **ionization** (ESI) **mass spectrometer** with the scanning-IR-**MALDI** data from the corresponding areas on the PVDF strip. The intensities of the **mass** profiles obtained by scanning-IR-**MALDI** reflect the amount of **peptides** present on the PVDF strip. The higher sensitivity of IR-**MALDI**-MS yielded **mass** information not detectable by ESI-MS. After the scanning-IR-**MALDI** experiment, the same membrane strip can be used directly for automated Edman degradation. Comparable initial and repetitive yields were obtained for blotted **peptides** with and without **matrix** incubation.

CC **Biochemical Methods - General *10050**
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Chemicals & Biochemicals
POLYVINYLIDENE FLUORIDE

IT Miscellaneous Descriptors
BIOCHEMISTRY AND BIOPHYSICS; HIGH-SENSITIVITY **PEPTIDE** MAPPING; MASS INFORMATION; METHODOLOGY; MICRO-LC; MICRO-LIQUID **CHROMATOGRAPHY**; **PEPTIDE** MAPPING METHOD; POLYVINYLIDENE FLUORIDE MEMBRANE

RN 24937-79-9 (POLYVINYLIDENE FLUORIDE)

L92 ANSWER 24 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1997:385360 BIOSIS
DN PREV199799684563
TI Sequencing of N-linked oligosaccharides directly from protein **gels** : In-**gel** deglycosylation followed by **matrix-assisted laser desorption/ionization** **mass spectrometry** and normal-phase high-performance liquid **chromatography**.
AU Kuester, Bernhard; Wheeler, Susan F.; Hunter, Ann P.; Dwek, Raymond A.; Harvey, David J.
CS Dep. Biochem., Oxford Glycobiol. Inst., Univ. Oxford, South Parks Rd., Oxford OX1 3QU UK
SO Analytical Biochemistry, (1997) Vol. 250, No. 1, pp. 82-101. ISSN: 0003-2697.
DT Article
LA English
AB A generally applicable, rapid, and sensitive method for profiling and sequencing of glycoprotein-associated N-linked oligosaccharides from protein gels was developed. The method employed sodium dodecyl sulfatepolyacrylamide gel electrophoresis (SDS-PAGE) for protein separation and purification and in-gel deglycosylation using PNGase F for glycan release. Profiles of the neutral glycans from bovine ribonuclease B, chicken ovalbumin, and human immunoglobulin G (IgG), as well as sialic acid-containing sugars (following esterification of the acidic groups) of bovine fetuin and bovine alpha-1-acid glycoprotein, were obtained by **matrix-assisted laser desorption/ionization mass spectrometry** (**MALDI** MS) and by normal-phase high-performance liquid **chromatography** following fluorescent labeling. Oligosaccharides were sequenced using specific exoglycosidases, and digestion products were analyzed by **MALDI** MS. Between 50 and 100 pmol (1.5 to 15 mu-g) of glycoprotein applied to the gel was sufficient to characterize its oligosaccharide contents. The identity of all glycoproteins investigated could be confirmed after deglycosylation by in-gel trypsin treatment followed by **MALDI** MS **mass** mapping and matching the measured molecular weights to a sequence database. The technique was used for the

characterization of the glycan moieties of human immunodeficiency virus recombinant gp120 (Chinese hamster ovary cells) and to monitor changes in the glycosylation of this glycoprotein when produced in the presence of a glucosidase I inhibitor. Furthermore, since heavy and light chains of IgG became separated by SDS-PAGE, it could be established that most glycans were associated with the heavy chains.

CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Carbohydrates *10068
Biophysics - General Biophysical Techniques *10504

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND BIOPHYSICS; GLYCOPROTEIN-ASSOCIATED N-LINKED OLIGOSACCHARIDES; HUMAN IMMUNODEFICIENCY VIRUS RECOMBINANT GP120; IMMUNOGLOBULIN G; IN-GEL DEGLYCOSYLATION; **MATRIX-ASSISTED LASER DESORPTION/IONIZATION MASS SPECTROMETRY**; METHODOLOGY; NORMAL-PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; PURIFICATION METHOD; SAMPLE PROCESSING METHOD; SDS-POLYACRYLAMIDE GEL ELECTROPHORESIS; SEPARATION METHOD; SEQUENCING

L92 ANSWER 25 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1997:243615 BIOSIS
DN PREV199799542818
TI Isolation and characterization of proteins from human **lymphocyte** nuclei using **matrix-assisted laser desorption/ionization** time-of-flight **mass spectrometry** and post-source decay analysis.
AU Nilsson, Carol L. (1); Murphy, Constance M.; Ekman, Rolf
CS (1) Dep. Neurochemistry, Univ. Goteborg, S-431 80 Molndal Sweden
SO Rapid Communications in Mass Spectrometry, (1997) Vol. 11, No. 6, pp. 610-612.
ISSN: 0951-4198.
DT Article
LA English
AB The cell nucleus plays an essential role in all aspects of cell function, including DNA replication, gene transcription, RNA processing and cell division. Within the cell nucleus there are many proteins and **peptides** that have regulatory roles. Although several higher molecular weight protein components (gt 30 kDa) have been identified and characterized, limited information is available for the lower molecular weight components. Nuclei from human peripheral blood lymphocytes were isolated and rapidly characterized by employing a strategy using reversed-phase high-performance liquid **chromatography**, tryptic digestion, and post-source decay analysis of matrix-assisted laser desorption/ionization (**MALDI**) ions in combination with database searches. Database searches utilizing molecular weight, proteolytic digest fragments, and **peptide** sequence results identified known proteins. The results illustrate the usefulness of **MALDI** as a tool in the characterization of low abundance proteins in the cell nucleus.

CC Cytology and Cytochemistry - Human *02508
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
Blood, Blood-Forming Organs and Body Fluids - Lymphatic Tissue and Reticuloendothelial System *15008

BC Hominidae *86215

IT Major Concepts
Biochemistry and Molecular Biophysics; Blood and Lymphatics (Transport and Circulation); Cell Biology; Methods and Techniques

IT Miscellaneous Descriptors
ANALYSIS; **ANALYTICAL METHOD**; BIOCHEMISTRY AND

BIOPHYSICS; BLOOD AND LYMPHATICS; CHARACTERIZATION; IMMUNE SYSTEM; ISOLATION; **MATRIX-ASSISTED LASER DESORPTION/IONIZATION** TIME-OF-FLIGHT **MASS SPECTROMETRY**; METHODOLOGY; NUCLEAR PROTEINS; PERIPHERAL BLOOD LYMPHOCYTES; POST-SOURCE DECAY ANALYSIS

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae)

ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L92 ANSWER 26 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1996:456719 BIOSIS
DN PREV199699179075
TI Determination of bacterial protein **profiles** by **matrix-assisted laser desorption/ionization mass spectrometry** with high-performance liquid **chromatography**.
AU Liang, Xiaoli; Zheng, Kefei; Qian, Mark G.; Lubman, David M. (1)
CS (1) Dep. Chem., Univ. Michigan, Ann Arbor, MI 48109-1055 USA
SO Rapid Communications in Mass Spectrometry, (1996) Vol. 10, No. 10, pp. 1219-1226.
ISSN: 0951-4198.
DT Article
LA English
CC Cytology and Cytochemistry - Animal *02506
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Physiology and Biochemistry of Bacteria *31000
Microbiological Apparatus, Methods and Media *32000
BC Bacteria - General Unspecified 05000
Lepidoptera *75330
IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Methods and Techniques; Physiology
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BACTERIAL PROTEIN PROFILING; BIOCHEMISTRY AND BIOPHYSICS; CAPILLARY HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; DETECTION; DISCRIMINATION; EXPRESSION MONITORING; EXPRESSION VECTOR; HSP27; **MATRIX-ASSISTED LASER DESORPTION/IONIZATION MASS SPECTROMETRY**; METHODOLOGY; PROTEIN; PURIFICATION METHOD; UV ABSORPTION DETECTOR

ORGN Super Taxa
Bacteria - General Unspecified: Eubacteria, Bacteria; Lepidoptera: Insecta, Arthropoda, Invertebrata, Animalia

ORGN Organism Name
bacteria (Bacteria - General Unspecified); SF9 (Lepidoptera): cell line

ORGN Organism Superterms
animals; arthropods; bacteria; eubacteria; insects; invertebrates; microorganisms

L92 ANSWER 27 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1996:391041 BIOSIS
DN PREV199699113397
TI **Matrix-assisted laser desorption ionization mass spectrometry** as a **complement** to internal protein sequencing.
AU Williams, Kenneth R.; Samandar, Suzy M.; Stone, Kathryn L.; Saylor, Melissa; Rush, John
CS Biotechnol. Resource Lab., Yale Univ., New Haven, CT USA
SO Walker, J. M. [Editor]. (1996) pp. 541-555. The protein protocols handbook.
Publisher: Humana Press Inc. Suite 808, 999 Riverview Drive, Totowa, New

Jersey 07512, USA.
ISBN: 0-89603-339-2 (paper), 0-89603-338-4 (cloth).
DT Book
LA English
CC Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Radiology (Medical Sciences)
IT Chemicals & Biochemicals
SECRETIN
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BOOK CHAPTER; GRAM-S; **PEPTIDE**-Y; PURIFICATION METHOD; REVERSE-PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; SECRETIN
RN 1393-25-5 (SECRETIN)

L92 ANSWER 28 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1996:375570 BIOSIS
DN PREV199699097926
TI Mass spectrometric characterization of glycosylated interferon-gamma variants separated by **gel** electrophoresis.
AU Mortz, Ejvind; Sareneva, Timo; Julkunen, Sophie Ii Haebelkka; Roepstorff, Peter (1)
CS (1) Dep. Molecular Bio., Odense Univ., Campusvej 55, DK-5230 Odense M Denmark
SO Electrophoresis, (1996) Vol. 17, No. 5, pp. 925-931.
ISSN: 0173-0835.
DT Article
LA English
AB Glycosylated proteins in polyacrylamide gels were characterized by **matrix-assisted laser desorption ionization mass spectrometry** (**MALDI**-MS) and glycosidase digestion. Sodium dodecyl sulfate-polyacrylamide get electrophoresis (SDS-PAGE) of natural, human interferon-y (IFN-gamma) showed two glycosylated variants with apparent molecular **masses** of 20 and 24 kDa. **MALDI**-MS of the intact IFN-gamma, electroeluted from the two bands, confirmed that these correspond to IFN-gamma molecules glycosylated at one or both of the two potential glycosylation sites, respectively. The **peptide** map obtained by **MALDI**-MS after digestion in the gel covers 92% of the IFN-gamma sequence and revealed an N-terminal pyroglutamate residue and one oxidized methionine residue. One glycosylated **peptide** was detected after treatment of the **peptide** mixture with neuraminidase, and the carbohydrate structure partially elucidated by sequential glycosidase digestion monitored by **MALDI**-MS. A second glycosylated **peptide**, due to a very heterogeneous glycan structure, could only be observed after separation of the **peptides** by high performance liquid **chromatography** (HPLC).
CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND MOLECULAR BIOPHYSICS; CHARACTERIZATION; GEL ELECTROPHORESIS; GLYCOSYLATED INTERFERON-GAMMA VARIANTS; HUMAN INTERFERON-GAMMA; **MATRIX-ASSISTED LASER DESORPTION IONIZATION MASS SPECTROMETRY**; METHODS AND TECHNIQUES; PURIFICATION METHOD

L92 ANSWER 29 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1996:375569 BIOSIS

DN PREV199699097925
TI Structural analysis and identification of **gel**-purified proteins, available in the femtomole range, using a novel **computer** program for **peptide** sequence assignment, by **matrix-assisted laser desorption ionization** -reflectron time-of-flight-**mass spectrometry**.
AU Gevaert, Kris; Verschelde, Jean-Luc; Puype, Magda; Van Damme, Jozef; Goethals, Marc; De Boeck, Stefan; Vandekerckhove, Joel (1)
CS (1) Flanders Interuniv. Inst. Biotechnol., Dep. Biochemistry, Fac. Med., Univ. Gent, Ledeganckstraat 35, B-9000 Gent Belgium
SO Electrophoresis, (1996) Vol. 17, No. 5, pp. 918-924.
ISSN: 0173-0835.
DT Article
LA English
AB A procedure is described for structural characterization and identification of proteins, purified by either one- or two-dimensional gel electrophoresis in the low picomole to femtomole range. The purified proteins are first detected in the primary gels by the sensitive reverse staining procedure described by Fernandez-Patron et al. (Anal. Biochem. 1995, 224, 203-211) and consecutively reeluted from combined gel pieces and concentrated in the tip of a Pasteur pipette in a secondary gel **matrix** consisting of either sodium dodecyl sulfate-polyacrylamide or agarose. The concentrated proteins are in-**matrix**-digested and the resulting **peptides** are separated by reverse-phase high performance liquid **chromatography** (HPLC) combined with microsequencing or analyzed by **matrix-assisted laser desorption ionization** - time of flight - **mass spectrometry**. Protein identification is based on sequence homology or on the **peptide mass** pattern. The matching **peptide** sequences can additionally be verified by matching their measured post-source decay spectra with the calculated fragmentation patterns of the isobaric candidate **peptides** appearing on the search list. This is done by a computer program referred to as MassFrag, described in this paper. We demonstrate that it is possible to identify protein that are only available in the femtomole range and whose sequences are stored in nonredundant protein databases or nucleotide and expressed sequence tag databases.
CC **Biochemical Methods - Proteins, Peptides and Amino Acids *10054**
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Miscellaneous Descriptors
ANALYTICAL METHOD; BIOCHEMISTRY AND MOLECULAR BIOPHYSICS; COMPUTER PROGRAM; IDENTIFICATION; MASSFRAG; **MATRIX-ASSISTED LASER DESORPTION IONIZATION**-REFLECTRON TIME-OF-FLIGHT-**MASS SPECTROMETRY**; METHODS AND TECHNIQUES; PICOMOLE TO FEMTOMOLE QUANTITY; PROTEIN; PURIFICATION METHOD; REVERSED-PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; SEQUENCE ASSIGNMENT METHOD; STRUCTURAL ANALYSIS

L92 ANSWER 30 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1996:375565 BIOSIS
DN PREV199699097921
TI Application of combined mass spectrometry and partial amino acid sequence to the identification of **gel**-separated proteins.
AU Patterson, Scott D. (1); Thomas, Didier; Bradshaw, Ralph A.
CS (1) Amgen Inc., Protein Structure, Amgen Cent., Mail Stop 14-2-E, 1840 DeHavilland Drive, Thousand Oaks, CA 91320-1789 USA
SO Electrophoresis, (1996) Vol. 17, No. 5, pp. 877-891.
ISSN: 0173-0835.
DT Article
LA English
AB The combined use of **peptide mass** information with amino acid sequence information derived by chemical sequencing or

mass spectrometry (MS)-based approaches provides a powerful means of protein identification. We have used a two-part strategy to identify proteins from nerve growth factor (NGF)-stimulated rat adrenal pheochromocytoma cell line PC-12 cell lysates that associate with the adaptor protein Shc (Shc homologous and collagen protein). Initial experiments with metabolically radiolabeled cell extracts separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) revealed a number of proteins that coimmunoprecipitated with anti-Shc antibody compared with control (unstimulated) cell extracts. The experiment was scaled up and cell lysate from NGF-stimulated PC-12 cells was applied to a glutathione-S-transferase (GST)-Shc affinity column, eluted, separated by SDS-PAGE and blotted to Immobilon-CD. The blotted proteins were proteolytically digested in situ, and the **masses** obtained from the extracted **peptides** were used in a **peptide-mass** search program in an attempt to identify the protein. Even if a strong candidate was found using this search, an additional step was performed to confirm the identification. The mixtures were fractionated by reversed-phase high-performance liquid **chromatography** (RP-HPLC) and subjected to chemical sequencing to obtain (partial) sequence information, or postsource decay (PSD-) **matrix-assisted laser-desorption ionization** (**MALDI**)-MS to obtain sequence-specific fragment ions. This data was used in a **peptide**-sequence tag search to confirm the identity of the proteins. This combined approach allowed identification of four proteins of M-r 43,000 to 200,000. In one case the identified protein clearly did not correspond to the radiolabeled band, but to a protein contaminant from the column. The advantages and pitfalls of the approach are discussed.

CC Cytology and Cytochemistry - Animal *02506
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biophysics - General Biophysical Techniques *10504
BC Muridae *86375
IT Major Concepts
Cell Biology; Methods and Techniques
IT Miscellaneous Descriptors
AFFINITY COLUMN **CHROMATOGRAPHY**; AMINO ACID SEQUENCING; **ANALYTICAL METHOD**; BIOCHEMISTRY AND MOLECULAR BIOPHYSICS; **MALDI**-MS; **MASS**; **MASS SPECTROMETRY**; METHODS AND TECHNIQUES; POST-SOURCE DECAY **MATRIX-ASSISTED LASER-DESORPTION IONIZATION MASS SPECTROMETRY**; PROTEIN; PURIFICATION METHOD; REVERSED-PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; RP-HPLC; SDS-POLYACRYLAMIDE GEL ELECTROPHORESIS
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
PC-12 (Muridae): cell line
ORGN Organism Superterms
animals; chordates; mammals; nonhuman mammals; nonhuman vertebrates; rodents; vertebrates

L92 ANSWER 31 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1995:403424 BIOSIS
DN PREV199598417724
TI Evaluation of mass spectrometric techniques for characterization of **engineered** proteins.
AU Roepstorff, Peter (1); Schram, Karl H.; Andersen, Jens S.; Rafn, Kate; Baldursson, Trausti; Kroll, Jenny; Poulsen, Kjeld; Knudsen, Jens; Kristiansen, Karsten
CS (1) Dep. Molecular Biol., Odense Univ., DK-5230 Odense M Denmark
SO Molecular Biotechnology, (1995) Vol. 4, No. 1, pp. 1-12.
ISSN: 1073-6085.
DT Article
LA English
AB Mass spectrometric characterization of engineered proteins has been examined using bovine recombinant Acyl-CoA-Binding Protein (rACBP),

(15N)-labeled rACBP, and a number of sequence variants of ACBP produced by site-directed mutagenesis. The mass spectrometric techniques include ESIMS and **MALDIMS** for analysis of the intact protein. **Peptide** maps have been obtained either by direct analysis of enzymatically derived mixtures by PDMS, ESIMS, and **MALDIMS** or by off- and on-line HPLC-mass spectrometry. ESIMS was found to be most accurate for analysis of intact proteins. The best sequence coverage in mapping was obtained by LC-ESIMS and by direct mixture analysis by **MALDIMS**. The latter technique was favorable in terms of sensitivity and speed. A general strategy for mass spectrometric characterization of engineered proteins is suggested.

CC Methods, Materials and Apparatus, General - Laboratory Methods *01004
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal 03506
Radiation - Radiation and Isotope Techniques *06504
Comparative Biochemistry, General *10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Replication, Transcription, Translation *10300
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - Methods *10804
Metabolism - Proteins, Peptides and Amino Acids *13012
Genetics of Bacteria and Viruses *31500

IT Major Concepts
Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Radiology (Medical Sciences)

IT Sequence Data
amino acid sequence; molecular sequence data

IT Miscellaneous Descriptors
ANALYTICAL METHOD; GENETIC ENGINEERING; HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; METHOD SENSITIVITY; METHODS; MOLECULAR BIOTECHNOLOGY; **PEPTIDE** MAPS; RADIOLABELING

L92 ANSWER 32 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1995:58848 BIOSIS
DN PREV199598073148
TI Analysis of two-dimensional **gel** proteins by mass spectrometry and microsequencing.
AU Henzel, William J.; Grimley, Christopher; Bourell, James H.; Billeci, Todd M.; Wong, Susan C.; Stults, John T.
CS Dep. Protein Chem., Genentech Inc., South San Francisco, CA 94080-4990 USA
SO Methods (Orlando), (1994) Vol. 6, No. 3, pp. 239-247.
ISSN: 1046-2023.
DT Article
LA English
AB A method for in situ digestion that allows high recovery of **peptides** at the low picomole level from two-dimensional gel electroblotted proteins is described. **Peptides** obtained from in situ digests were analyzed by **matrix-assisted laser desorption/ ionization** and electrospray **ionization mass spectrometry. Mass** analysis of **peptides** from digestion of single 2-D gel spots provided information sufficient to identify proteins from a protein sequence database using a fragment ion searching algorithm. Separation of these **peptides** by capillary HPLC allowed high recovery for **peptide** sequence analysis. The use of a microreaction cartridge in a gas-phase sequencer with a 37-min fast cycle enabled **peptide** sequencing by Edman degradation at the subpicomole level.
CC Radiation - Radiation and Isotope Techniques *06504

Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Radiology (Medical Sciences)
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CAPILLARY HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**; EDMAN DEGRADATION; ELECTROSPRAY **IONIZATION MASS SPECTROMETRY**; **MATRIX-ASSISTED LASER DESORPTION IONIZATION**; SEQUENCE ANALYSIS

L92 ANSWER 33 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1995:29901 BIOSIS
DN PREV199598044201
TI **Micromethods** for protein structure analysis.
AU Shively, John E.
CS City of Hope, Duarte, CA USA
SO Methods (Orlando), (1994) Vol. 6, No. 3, pp. 207-212.
ISSN: 1046-2023.
DT Article
LA English
CC Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques; Radiology (Medical Sciences)
IT Miscellaneous Descriptors
ANALYTICAL METHODS COMPARISON; CAPILLARY ELECTROPHORESIS; ELECTROSPRAY **IONIZATION**; LIQUID **CHROMATOGRAPHY**; **MASS SPECTROMETRY**; **MATRIX-ASSISTED LASER DESORPTION IONIZATION**-TIME-OF-FLIGHT; PURIFICATION METHODS COMPARISON; SECONDARY ION **MASS SPECTROMETRY**; SEQUENCE ANALYSIS

L92 ANSWER 34 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1994:266063 BIOSIS
DN PREV199497279063
TI Identification of proteins in polyacrylamide **gels** by mass spectrometric **peptide** mapping combined with database search.
AU Mortz, Ejvind (1); Vorm, Ole (1); Mann, Matthias; Roepstorff, Peter (1)
CS (1) Dep. Mol. Biol., Odense Univ., Campusvej 55, 5230 Odense M Denmark
SO Biological Mass Spectrometry, (1994) Vol. 23, No. 5, pp. 249-261.
ISSN: 1052-9306.
DT Article
LA English
AB **Mass spectrometric peptide** mapping of proteins separated by one-dimensional sodium dodecyl sulphate polyacrylamide gel electrophoresis has been investigated. The best results are obtained after blotting of the proteins onto polyvinylidene difluoride membranes followed by enzymatic digestion of the protein on the membrane. The **peptide** maps were investigated in terms of completeness and applicability for protein identification using a previously developed database search program as well as for the possibility for full characterization of covalent modifications in the proteins. The most complete **peptide** maps were obtained when the proteins were reduced and alkylated on the membrane prior to enzymatic digestion followed by separation of the resulting mixture by high performance liquid **chromatography** prior to **mass spectrometric** analysis. Such **peptide** maps cover up to 98% or the sequence and consequently may allow complete characterization of post-translational

modifications in proteins for which the amino acid sequence is known. The fastest and most sensitive procedure to obtain **peptide** maps sufficient for protein identification was direct analysis of the extracted **peptide** mixture by **matrix-assisted laser desorption ionization** (**MALDI**) **mass spectrometry**. The use of external and internal calibration of **MALDI** spectra for database searches is evaluated as well as the possibility of including a post-calibration routine within the search program.

CC General Biology - Information, Documentation, Retrieval and Computer Applications *00530
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504

IT Major Concepts
Biochemistry and Molecular Biophysics; Information Studies; Methods and Techniques

IT Chemicals & Biochemicals
POLYACRYLAMIDE

IT Miscellaneous Descriptors
ANALYTICAL METHOD

RN 9003-05-8 (POLYACRYLAMIDE)

L92 ANSWER 35 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1992:184606 BIOSIS
DN BA93:95556
TI **ANALYSIS** OF **SYNTHETIC PEPTIDES** USING **MATRIX-ASSISTED LASER DESORPTION IONIZATION MASS SPECTROMETRY.**
AU STEINER V; BORNSEN K O; SCHAER M; GASSMANN E; HOFFSTETTER-KUHN S; RINK H; MUTTER M
CS ANALYTICAL RES., K-127/132, CIBA-GEIGY LTD., CH-4002 BASEL, SWITZ.
SO PEPT RES, (1992) 5 (1), 25-29.
CODEN: PEREEO. ISSN: 1040-5704.
FS BA; OLD
LA English
AB Matrix-assisted laser desorption ionization mass spectroscopy (LDI MS), a novel method for analysis of large molecules, has been used for characterization of synthetic **peptides** and their by-products. The potential of LDI MS is demonstrated by analyzing crude synthetic **peptides** representing typical members of newly designed **peptides** and proteins. In the first case, a fragment condensation reaction yielding a highly hydrophobic six-helix bundle template-assembled synthetic protein (TASP) is monitored. Then, a crude 19-mer **peptide** designed to adopt an amphiphilic .alpha.-helical structure and its by-products from SPPS are identified. Finally, analysis of crude hirulog-1, a 20-mer **peptide** designed as a thrombin inhibitor, using C18 reversed phase high performance liquid **chromatography** (RP HPLC), capillary electrophoresis (CE) and LDI MS, manifests the potential of the latter method.

CC Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504

IT Miscellaneous Descriptors
AMINO ACIDS REVERSED PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY**

L92 ANSWER 36 OF 36 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1991:427594 BIOSIS
DN BA92:83759
TI ANALYTICAL **APPLICATIONS** OF **MATRIX-ASSISTED LASER DESORPTION** AND **IONIZATION MASS SPECTROMETRY.**
AU BORNSEN K O; SCHAR M; GASSMANN E; STEINER V
CS CENTRAL ANALYTICAL DEP., CIBA-GEIGY LTD, CH-4002 BASEL, SWITZ.

SO BIOL MASS SPECTROM, (1991) 20 (8), 471-478.
CODEN: BIMSEH. ISSN: 1052-9306.
FS BA; OLD
LA English
AB **Matrix-assisted laser desorption ionization mass spectrometry** (LDI-MS) has been used successfully for monitoring and quality of control of a protein synthesis and for identification of by-products. In a first example it is shown that LDI-MS can be used to determine the amount and **mass** of the protein and the impurities in a commercially available protein product. The second example describes a protein synthesis where LDI-MS is the analytical method of choice which allows determination of the endpoint of the synthesis, the purity of the product and the obstained by-products. As a third example of synthesis of hirudin by recombinant DNA technology is shown where degraded r-hirudin with one or more missing amino acids are easily detected and distinguished from the complete r-hirudin. The **mass** determination and identification of the missing amino acids is presented. The results of LDI-MS are compared with results of state-of-the art analytical methods like reversed-phase high-performance liquid **chromatography**, sodium dodecyl sulphate-polyacrylarmide gel electrophoresis, and capillary electrophoresis.
CC Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Techniques *10504
IT Miscellaneous Descriptors
PROTEIN SYNTHESIS REVERSED-PHASE HIGH PERFORMANCE LIQUID **CHROMATOGRAPHY** SDS-POLYACRYLAMIDE GEL ELECTROPHORESIS CAPILLARY ELECTROPHORESIS

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FILE 'HCAPLUS' ENTERED AT 09:07:30 ON 30 DEC 1999
L93 4790 S L61
L94 805 S L93 AND ?CHROMATOG?
L95 278 S L94 AND ?PEPTIDE?
L96 6 S L95 AND P/DT
L97 4 S L96 NOT FORSSMANN ?/AU
L98 2 S L97 AND MOLECULAR ()(WEIGHT OR MASS)

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L99          92 S L95 AND MOLECULAR ()(WEIGHT OR MASS)
L100         89 S L99 NOT L96
L101         23 S L100 AND (?MICROBOR? OR ?ELECTROSPRAY? OR ?ELECTRO SPRAY? OR
L102         12 S L100 AND REVERSE
L103         33 S L101,L102
L104         33 S L103 NOT FORSMAN?/AU
L105          8 S L104 AND 9/SC
L106         10 S L98,L105
L107          6 S L106 NOT (ASPERG? OR BRAUN OR OCULAR OR CALRETICUL?)/TI
L108          7 S L98,L107
L109          1 S L108 NOT L107

     FILE 'HCAPLUS' ENTERED AT 09:15:32 ON 30 DEC 1999

=> d all tot l108

L108 ANSWER 1 OF 7  HCAPLUS  COPYRIGHT 1999 ACS
AN   1999:189279  HCAPLUS
DN   130:220168
TI   Processes and kits for mass spectrometric determination of
     polypeptides
IN   Little, Daniel; Koster, Hubert; Higgins, G. Scott; Lough, David
PA   Sequenom, Inc., USA
SO   PCT Int. Appl., 134 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  G01N033-68
CC   9-5 (Biochemical Methods)
     Section cross-reference(s): 3, 14, 33
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   WO 9912040         A2   19990311      WO 1998-US18311  19980902
     WO 9912040         A3   19990902
         W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
             DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG,
             KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
             NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
             UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
             FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
             CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 9891298         A1   19990322      AU 1998-91298    19980902
PRAI US 1997-922201   19970902
     WO 1998-US18311  19980902
AB   A process for detg. the identity of a target polypeptide using
     mass spectroscopy is provided.  Depending on the target
     polypeptide to be identified, a process as disclosed can be used,
     for example, to diagnose a genetic disease or chromosomal abnormality, a
     predisposition to a disease or condition, or infection by a pathogenic
     organism; or for detg. identity or heredity.  Kits for performing the
     disclosed processes also are provided.  Human genomic DNA, extd. from
     blood of patients with spinal cerebellar ataxia 1, was amplified by PCR
     using forward and reverse primers contg. the T7 promoter sequence and a
     sequence encoding the His-6 tag peptide, resp., and hybridizing
     to sequences located on either side of the CAG trinucleotide repeat.  The
     amplified DNA was subjected to in vitro transcription and translation, and
     the target polypeptides were isolated on a nickel
     chromatog. column.  Mass spectrometric anal. of the
     polypeptides indicated that these peptides had
     mol. masses of 8238.8, 8865.4, and 8993.6 Da,
     corresponding to 10, 15, or 16 CAG (Asn) repeats.  The polypeptide
     encoded by the nucleic acid from the fourth patient, having and unknown
     no. of trinucleotide repeats, had a mol. mass of
     8224.8 Da.  While this value does not correspond exactly with a unit no.
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of repeats (10 is the closest), it is consistent with detection of a point mutation; i.e. the -14 Da shift for this **polypeptide** corresponds to an Ala to Gly mutation due to a C to G mutation in one of the repeats.

ST mass spectrometry detn protein; spinocerebellar ataxia CAG trinucleotide repeat protein mass spectrometry

IT Genes (animal)
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(BRCA2, target **polypeptide** encoded by allelic variant of; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Nervous system diseases
(Machado-Joseph, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Spinal muscular atrophy
(X-linked spinal and bulbar muscular atrophy, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Animal tissue
Body fluid
(as test sample; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Amino acids, properties
RL: PEP (Physical, engineering or chemical process); PRP (Properties); PROC (Process)
(cleavage of, from terminus of **polypeptide** for sequence detn.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Brain diseases
(dentatorubral-pallidoluysian atrophy, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Transplant (organ)
(detn. of compatibility in; processes and kits for mass spectrometric detn. of **polypeptides**)

IT DNA sequences
Protein sequences
(for CAG trinucleotide repeat region of human with spinocerebellar ataxia 1; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Electric charge
(heterogeneity, redn. of, before mass spectrometry; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Enzymes, uses
RL: CAT (Catalyst use); USES (Uses)
(in cleavage of amino acids from terminus of **polypeptide** for sequence detn.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Point mutation
(in gene for target **polypeptide**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Avidins
RL: ARG (Analytical reagent use); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(in isolation of biotin-tagged target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Nucleic acid amplification (method)
Transcription (genetic)
Translation (genetic)
(in obtaining target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)

(in obtaining target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Cation exchangers
(in redn. of charge heterogeneity before mass spectrometry; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Mass
(molar, detn. of; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Immobilization (molecular)
(of target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Promoter (genetic element)
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(primer contg., in obtaining target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Electrospray ionization mass spectrometry
Forensic analysis
Fourier transform ion cyclotron resonance mass spectrometry
Genotyping (method)
Ion spray mass spectrometry
Ion trap mass spectrometry
Mass spectrometry
Matrix-assisted laser desorption ionization mass spectrometry
Paternity testing
Protein sequence analysis
Quadrupole mass spectrometry
Test kits
Thermospray ionization mass spectrometry
Time-of-flight mass spectrometry
(processes and kits for **mass spectrometric** detn. of **polypeptides**)

IT Proteins (general), analysis
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(processes and kits for mass spectrometric detn. of **polypeptides**)

IT Muscle atrophy
(spino bulbar, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Ataxia
(spinocerebellar, type 1, target **polypeptides** encoded by CAG trinucleotide repeats assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Haemophilus influenzae
(tag **peptide** from, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT c-myc gene (animal)
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(tag **peptide** from, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Hemagglutinins
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(tag **peptide** of, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT **Peptides**, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(tag, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Diseases (animal)
(target **polypeptide** encoded by allelic variant assocd. with condition or; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Aging (animal)
Huntington's disease
Prostatic tumors
Transplant rejection
(target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Dystrophin
MHC antigens
p53 (protein)
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(target **polypeptide** encoded by allelic variant of gene for; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Chromosomes
(target **polypeptide** encoded by allelic variant of polymorphic region of; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Polymorphism (genetic)
(target **polypeptide** encoded by allelic variant of, of chromosome; processes and kits for mass spectrometric detn. of **polypeptides**)
IT APC gene (animal)
BRCA1 gene (animal)
CFTR gene (animal)
Mitochondrial DNA
Oncogenes (animal)
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(target **polypeptide** encoded by allelic variant of; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Alleles
(target **polypeptide** encoded by, of polymorphic region of chromosome; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Bacteria (Eubacteria)
Fungi
Protista
Virus
(target **polypeptide** from infectious; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Infection
(target **polypeptide** from organism causing; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Coupling agents
(target **polypeptides** immobilized to solid support through cleavable; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Light
(target **polypeptides** immobilized to solid support through linker cleavable with; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Acids, uses
RL: NUU (Nonbiological use, unclassified); USES (Uses)
(target **polypeptides** immobilized to solid support through linker cleavable with; processes and kits for mass spectrometric detn. of **polypeptides**)
IT Antibodies
RL: ARG (Analytical reagent use); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)

(target **polypeptides** isolation with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Genes
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(transcription and translation of, in obtaining target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT RNA
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(translation of, in obtaining target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Fragile X syndrome
(type A, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Myotonic dystrophy
(type I, target **polypeptide** encoded by allelic variant assocd. with; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Protein conjugates
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(with tag **peptide**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT Hemoglobins
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(.beta.-chain, target **polypeptide** encoded by allelic variant of gene for; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 221149-87-7
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 25104-18-1, Polylysine 25212-18-4, Polyarginine 26062-48-6, Polyhistidine 50812-37-8, Glutathione-S-transferase
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(as tag **peptide**, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 58-85-5, Biotin
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(as tag, target **polypeptide** contg.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 221111-73-5
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(forward primer for PCR amplification of trinucleotide repeats assocd. with spinal cerebellar ataxia 1; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 9031-94-1, Aminopeptidase 9031-98-5, Carboxypeptidase
RL: CAT (Catalyst use); USES (Uses)
(in cleavage of amino acids from terminus of **polypeptide** for sequence detn.; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 9001-92-7, Endopeptidase
RL: CAT (Catalyst use); USES (Uses)
(in cleavage of **polypeptide**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 9013-20-1, Streptavidin
RL: ARG (Analytical reagent use); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(in isolation of biotin-tagged target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 7440-02-0D, Nickel, chelates with solid supports 7440-48-4D, Cobalt, chelates with solid supports 7440-50-8D, Copper, chelates with solid supports 7440-66-6D, Zinc, chelates with solid supports
RL: ARG (Analytical reagent use); BPR (Biological process); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
(in isolation of tagged target **polypeptides**; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 207398-06-9P
RL: BYP (Byproduct); PREP (Preparation)
(in prepn. of photocleavable linker that can be used in oligonucleotide synthesis; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 108-24-7 498-02-2 627-18-9, 3-Bromo-1-propanol 7697-37-2, Nitric acid, reactions 42454-06-8, 5-Hydroxy-2-nitrobenzaldehyde 89992-70-1, 2-Cyanoethyl-N,N-diisopropylchlorophosphoramidite
RL: RCT (Reactant)
(in prepn. of photocleavable linker that can be used in oligonucleotide synthesis; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 187794-03-2P 207298-34-8P 207298-35-9P 207298-36-0P 207298-37-1P 207298-39-3P 207298-40-6P 207298-41-7P 207298-42-8P 207298-43-9P 221112-24-9P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation)
(in prepn. of photocleavable linker that can be used in oligonucleotide synthesis; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 221149-86-6
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 207298-33-7P 207298-38-2P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of, as photocleavable linker that can be used in oligonucleotide synthesis; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 221111-74-6
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(reverse primer for PCR amplification of trinucleotide repeats assocd. with spinal cerebellar ataxia 1; processes and kits for mass spectrometric detn. of **polypeptides**)

IT 9001-25-6P, Blood-coagulation factor VII 9001-28-9P, Factor IX 9016-12-0P, Hypoxanthine guanine phosphoribosyl transferase 9030-40-4P
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(target **polypeptide** encoded by allelic variant of gene for; processes and kits for mass spectrometric detn. of **polypeptides**)

L108 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1999:87094 HCAPLUS
DN 130:264395
TI Characterization of **peptides** from Aplysia using **microbore** liquid **chromatography** with **matrix-assisted laser desorption/ionization**

time-of-flight **mass spectrometry** guided purification
AU Floyd, Philip D.; Li, Lingjun; Moroz, Tatiana P.; Sweedler, Jonathan V.
CS Department of Chemistry and Beckman Institute, University of Illinois at Urbana-Champaign, Urbana, IL, 61801, USA
SO J. Chromatogr., A (1999), 830(1), 105-113
CODEN: JCRAEY; ISSN: 0021-9673
PB Elsevier Science B.V.
DT Journal
LA English
CC **9-16** (Biochemical Methods)
AB Liq. **chromatog.** (LC) has been used extensively for the sepn. and isolation of **peptides** due to its high selectivity and peak capacity. · An approach combining **microbore** LC with **matrix-assisted laser desorption/ ionization** time-of-flight **mass spectrometry** (**MALDI**-MS) detection is described to identify **peptides** in cells and guide the purifn. of **peptides** from the marine mollusc Aplysia californica. Direct **MALDI**-MS of neurons and processes provides **mol. mass** information for unknown **peptides** with almost no sample prepn., and LC-**MALDI**-MS allows the isolation and purifn. of these **peptides** from pooled samples, thus enabling new putative **neuropeptides** to be isolated from complex cellular samples. Both direct **MALDI**-MS and LC-**MALDI**-MS are compared in terms of detecting **peptides** from neuronal samples. Using both approaches, two peaks from Aplysia californica connectives having **mol. masses** of 5013 and 5021 have been isolated, partially sequenced and identified as novel collagen-like **peptides.**
ST **neuropeptide** collagen purifn Aplysia LC **MALDI** TOF
IT Aplysia californica
Ganglion
Liquid **chromatography-mass spectrometry**
Matrix-assisted laser desorption ionization mass spectrometry
Mollusk (Mollusca)
Purification
Sample preparation
Time-of-flight **mass spectrometry**
(characterization of **peptides** from Aplysia using **microbore** liq. **chromatog.** with **matrix-assisted laser desorption/ ionization** time-of-flight **mass spectrometry** guided purifn.)
IT Collagens, analysis
Neuropeptides
RL: ANT (Analyte); BOC (Biological occurrence); PUR (Purification or recovery); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(characterization of **peptides** from Aplysia using **microbore** liq. **chromatog.** with **matrix-assisted laser desorption/ ionization** time-of-flight **mass spectrometry** guided purifn.)

L108 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1998:675839 HCAPLUS
DN 129:272631
TI Application of capillary electrophoresis, liquid **chromatography, electrospray-mass spectrometry,** and **matrix-assisted laser desorption/ ionization** - time of flight - **mass spectrometry** to the characterization of recombinant human erythropoietin
AU Zhou, Guo-Hua; Luo, Guo-An; Zhou, Yong; Zhou, Ke-Yu; Zhang, Xiao-Dano; Huang, Le-Qun
CS Department Chemistry, Tsinghua University, Beijing, 100084, Peop. Rep. China

SO Electrophoresis (1998), 19(13), 2348-2355
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
CC **9-16** (Biochemical Methods)
AB High performance capillary electrophoresis (HPCE), high performance liq. **chromatog.** (HPLC), **matrix-assisted laser desorption/ionization** - time of flight - **mass spectrometry** (**MALDI**-TOF-MS), online CE-**electrospray ionization-mass spectrometry** (CE-ESI-MS) and online LC-ESI-MS have been employed to characterize a heterogeneous glycoprotein, recombinant human erythropoietin (rHuEPO) expressed from Chinese hamster ovary (CHO) cells. The anal. was demonstrated through 2 specific levels of detail: the intact protein and tryptic digests of the protein. 6 Glycoforms of rHuEPO were sepd. by HPCE; seventeen tryptic fragments in a total of 21 nonglycosylated and glycosylated **peptides** were characterized; the O-linked **glycopeptides** were analyzed directly by CE-ESI-MS and LC-ESI-MS. In particular, 4 glycans of O-acetylation of sialic acid were identified in the O-linked glycosylated fragments. The **mol. wt.** of rHuEPO was accurately detd. by **MALDI**-TOF-MS.
ST erythropoietin HPLC **MALDI** mass spectrometry electrophoresis; capillary electrophoresis HPLC **MALDI** MS erythropoietin
IT Capillary electrophoresis
Electrospray ionization mass spectrometry
HPLC
Matrix-assisted laser desorption ionization mass spectrometry
(application of capillary electrophoresis, liq. **chromatog.**, **electrospray-mass spectrometry**, and **matrix-assisted laser desorption/ionization** - time of flight - **mass spectrometry** to the characterization of recombinant human erythropoietin)
IT 11096-26-7, Erythropoietin
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(recombinant; application of capillary electrophoresis, HPLC, **electrospray-mass spectrometry**, and **matrix-assisted laser desorption/ionization** - time of flight - **mass spectrometry** to the characterization of recombinant human erythropoietin)

L108 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1998:252543 HCAPLUS
DN 129:25221
TI Analysis of human serum albumin variants by mass spectrometric procedures
AU Amoresano, Angela; Andolfo, Annapaola; Siciliano, Rosa Anna; Cozzolino, Rosaria; Minchiotti, Lorenzo; Galliano, Monica; Pucci, Piero
CS Centro Internazionale di Servizi di Spettrometria di Massa, Naples, 80131, Italy
SO Biochim. Biophys. Acta (1998), 1384(1), 79-92
CODEN: BBACAQ; ISSN: 0006-3002
PB Elsevier Science B.V.
DT Journal
LA English
CC **9-5** (Biochemical Methods)
AB A new strategy for the structural characterization of human albumin variants has been developed which makes extensive use of **mass spectrometric** methodologies. The rationale behind the method is to provide a rapid and effective screening of the entire albumin structure. The first step in this strategy consists in the attempt to det. the accurate **mol. mass** of the intact variant by

electrospray mass spectrometry often providing a first indication on the presence of the variant. An HPLC procedure has been developed to isolate all the seven fragments generated by CNBr hydrolysis of HSA in a single **chromatog.** step. A rapid screening of the entire albumin structure is achieved by the ESMS anal. of the **peptide** fragments and the protein region(s) carrying the structural abnormality is identified by its anomalous **mass** value(s). **Mass** mapping of the corresponding CNBr **peptide**, either by Fast Atom Bombardment **Mass Spectrometry** (FABMS) or by **Matrix Assisted Laser Desorption Ionisation Mass Spectrometry** (**MALDIMS**), leads to the definition of the site and the nature of the variation. This combined strategy was applied to the structural characterization of three HSA genetic variants and provided to be an effective procedure for the rapid assessment of their structural modifications showing considerable advantages over the classical approach.

ST albumin variant conformation mass spectrometry

IT Conformation
Mass spectrometry
Matrix-assisted laser desorption ionization mass spectrometry
(anal. of human serum albumin variants by **mass spectrometric** procedures)

IT Albumins, properties
RL: PRP (Properties)
(anal. of human serum albumin variants by mass spectrometric procedures)

L108 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1997:514749 HCAPLUS
DN 127:202243
TI An introduction to **electrospray ionization** and **matrix-assisted laser desorption/ ionization mass spectrometry**: essential tools in a modern biotechnology environment
AU Hop, Cornelis E. C. A.; Bakhtiar, Ray
CS Merck Research Laboratories, Department of Drug Metabolism, Rahway, NJ, 07065-0900, USA
SO Biospectroscopy (1997), 3(4), 259-280
CODEN: BIOSFS; ISSN: 1075-4261
PB Wiley
DT Journal; General Review
LA English
CC **9-0** (Biochemical Methods)
Section cross-reference(s): 1, 64
AB A review with many refs. The tremendous progress in biochem. and biotechnol. has been made possible in part by recent advances in anal. methods, in particular **mass spectrometry**. With the introduction of **electrospray ionization** (ESI) and **matrix-assisted laser desorption/ ionization** (**MALDI**), **mass spectrometry** allowed the detn. of the **mol. wt.** of **peptides** and proteins with a much greater accuracy than achievable by traditional methods such as SDS-PAGE and biogel **chromatog.** In addn., these **mass spectrometry** expts. have become routine and can be performed within minutes. ESI and **MALDI** (in combination with enzymic methods) can also provide vital structural data such as the amino acid sequence and the sites of posttranslational modifications for **peptides** and proteins with a sensitivity that competes favorably with other methods. The use of ESI and **MALDI** is not limited to **peptides** and proteins; anal. of oligonucleotides and oligosaccharides has been simplified by these techniques as well. For information about structurally significant noncovalent interaction between various types of biomols., ESI is probably one of the most convenient methods. Not surprisingly, we anticipate that the **mass**

spectrometers with these **ionization** capabilities will soon become std. equipment in all pharmaceutical and biotechnol. labs.
ST review **electrospray ionization matrix assisted; laser desorption mass spectrometry** biotechnol review
IT Biotechnology
Electrospray ionization mass spectrometry
Matrix-assisted laser desorption ionization mass spectrometry
(introduction to **electrospray ionization** and **matrix-assisted laser desorption/ionization mass spectrometry**: essential tools in a modern biotechnol. environment)

L108 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1997:85147 HCAPLUS
DN 126:86519
TI Enzyme system comprising ferulic acid esterase activity from Aspergillus
IN Michelsen, Birgit; De Vries, Ronald Peter; Visser, Jacob; Soe, Jorn Borch; Poulsen, Charlotte Horsmans; Zargahi, Masoud R.
PA Danisco A/S, Den.
SO Brit. UK Pat. Appl., 63 pp.
CODEN: BAXXDU
DT **Patent**
LA English
IC ICM C12N009-18
ICS C12N001-15; C12N015-55; C12N015-62
ICI C12N015-55, C12R001-66, C12R001-685, C12R001-69
CC 7-2 (Enzymes)
Section cross-reference(s): 3, 17
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
GB 2301103	A1	19961127	GB 1995-10370	19950523

AB An ferulic acid esterase (FAE) enzyme system is described that is useful for prepg. food and feed. One enzyme of that system is obtainable from the com. prepn. Pektolase CA from Aspergillus niger by **chromatog**. on anion-exchange DEAE-Sepharose FF and Phenyl-Sepharose HiLoad, gel filtration on Sephacryl HiLoad, and **chromatog**. on MonoQ HR 5/5 anion-exchange column. That enzyme has the following characteristics: a **mol. wt.** of 29-36 kDa as measured on a SDS-Phastgel (RTM) (10-15%) or about 30 kDa as measured by **MALDI**; a pI value of 3-4; ferulic acid esterase activity; a pH optimum of about 5 when Me ferulate is used as a substrate; and a temp. optimum of 50-60.degree. when MeFA is used as a substrate. The enzyme may be obtained by recombinant techniques. PCR screening of an Aspergillus genomic library with degenerate primers based on FAE tryptic **peptide** sequences yielded a PCR fragment encoding 77 amino acids of the enzyme. In the enzyme system, the esterase may be fused to a protein or enzyme, esp. a polysaccharide modifying enzyme. The effect of adding glucose oxidase/peroxidase and FAE to weak wheat flour was investigated by measuring the strength and extensibility of a dough prepd. from the flour. FAE can also be used to hydrolyze water-insol. wheat bran pentosans, for the partial breakdown of cell wall material in feed and food prepn., and to prep. vanillin from ferulic acid-contg. material such as sugar beet and corn cob meal.
ST ferulic acid esterase Aspergillus; food prepn ferulic acid esterase; feed prepn ferulic acid esterase; sequence ferulic acid esterase gene Aspergillus
IT Antioxidants
Aspergillus
Aspergillus niger
Bakery products
Dough
Feed

Food
(enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Antibodies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Genes (microbial)
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Corncob
Pentosans
Sugar beet
Wheat bran
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(hydrolysis by enzyme prepn.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Protein sequences
(of ferulic acid esterase activity from Aspergillus)

IT DNA sequences
(of gene for ferulic acid esterase activity from Aspergillus)

IT Enzymes, biological studies
RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
(oxidizing, food/feed applications of ferulic acid esterase in combination with; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Enzymes, biological studies
RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
(polysaccharide-degrading, food/feed applications of ferulic acid esterase in combination with; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Flavoring materials
(prepn. by enzyme system contg.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Fungi
Plant (Embryophyta)
Yeast
(recombinant host for enzyme prodn.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Genetic vectors
Plasmid vectors
(recombinant prepn. of enzyme; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT Phenols, biological studies
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(release from plant substrates by enzyme prepn.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 185703-92-8 185703-93-9
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PCR primer; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 185702-86-7P 185703-06-4P 185703-08-6P 185765-98-4P
RL: BPN (Biosynthetic preparation); FFD (Food or feed use); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 134712-49-5P, Ferulate esterase
RL: BPN (Biosynthetic preparation); FFD (Food or feed use); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 9000-82-2, Acetyl esterase 9001-37-0, Glucose oxidase 9001-92-7, Proteinase 9003-99-0, Peroxidase 9015-78-5, Glucanase 9032-75-1,

Pectinase 37278-89-0, Xylanase 37325-54-5, Arabanase 131384-64-0, Rhamnogalacturonase
RL: FFD (Food or feed use); BIOL (Biological study); USES (Uses)
(food/feed applications of ferulic acid esterase in combination with; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 9040-27-1, Arabinoxylan
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(hydrolysis by enzyme prepn.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 185703-07-5P
RL: BPN (Biosynthetic preparation); FFD (Food or feed use); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; enzyme system comprising ferulic acid esterase activity from Aspergillus)

IT 121-33-5P, Vanillin
RL: IMF (Industrial manufacture); PREP (Preparation)
(prepn. by enzyme system contg.; enzyme system comprising ferulic acid esterase activity from Aspergillus)

L108 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 1999 ACS
AN 1995:545970 HCAPLUS
DN 122:285871
TI Mass spectrometric **peptide** and protein charting
AU Feistner, Gottfried J.; Faull, Kym F.; Barofsky, Douglas F.; Roepstorff, Peter
CS Beckman Res. Inst. of the City of Hope, Duarte, CA, USA
SO J. Mass Spectrom. (1995), 30(4), 519-30
CODEN: JMSPFJ; ISSN: 1076-5174
DT Journal
LA English
CC **9-5** (Biochemical Methods)
AB Six years after coining the term '**mass spectrometric** (MS) **peptide** charting' for the component anal. of **peptide** mixts. in a whole tissue, body fluid, or an ext. thereof, the authors offer the current perspective of this field. **Matrix -assisted laser desorption/ ionization** and **electrospray ionization** have replaced plasmas **desorption** and fast atom bombardment as **ionization** methods of choice. At the same time, the upper **mass** range has been extended to now include most **peptides** and proteins of interest to reach on cell-cell communications. In addn. to qual. aspects, quant. applications of MS charting have become important. In combination with new database search algorithms, online liq. **chromatog.**-tandem **mass spectrometry** promises greater dividends from MS charting than are achievable with **mol. mass** matching alone. The authors discuss what is and is not yet possible, and consider foreseeable yeas for overcoming and current limitations. The intent is to encourage researchers in the biol. and medical sciences to take advantage of this powerful methodol. in their various fields of endeavor.
ST mass spectrometry **peptide** protein charting
IT Mass spectrometry
(mass spectrometric **peptide** and protein charting)
IT **Peptides**, analysis
Proteins, analysis
RL: ANT (Analyte); ANST (Analytical study)
(mass spectrometric **peptide** and protein charting)